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UTILITY PATENT APPLICATION TRANSMITTAL <small>Only for new nonprovisional applications under 37 CFR 1.53(h)</small>		Attorney Docket No. 08010137US07	
		First Named Inventor or Application Identifier	
Title Method of Determining the Presence of a Trait in a Plant by Transfecting a Nucleic Acid Sequence of a Non-Plant Donor Into a Host Plant in a Positive Orientation			
Express Mail Label No. EL273178733US			

APPLICATION ELEMENTS <small>See MPEP chapter 600 concerning utility patent application contents</small>	ADDRESS TO: Assistant Commissioner for Patents Box Patent Application Washington, DC 20231
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1. <input checked="" type="checkbox"/> *Fee Transmittal Form (Form PTO-1082) <small>(Submit an original and a duplicate for fee processing)</small> 2. <input checked="" type="checkbox"/> Specification [Total Pages 85] <small>(preferred arrangement set forth below)</small> - Descriptive title of the Invention - Cross References to Related Applications - Statement Regarding Fed sponsored R&D - Reference to Microfiche Appendix - Background of the Invention - Brief Summary of the Invention - Brief Description of the Drawings (if filed) - Detailed Description - Claims - Abstract of the Disclosure 3. <input checked="" type="checkbox"/> Drawing(s) (35 USC 113) [Total Sheets 23] 4. Oath or Declaration [Total Pages 1] a. <input type="checkbox"/> Newly executed (original or copy) b. <input type="checkbox"/> Copy from a prior application (37 CFR 1.63(d)) <small>(for continuation/divisional with Box 17 completed)</small> <small>[Note Box 5 below]</small> i. <input type="checkbox"/> DELETION OF INVENTOR(S) <small>Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).</small> 5. <input type="checkbox"/> Incorporation By Reference (useable if Box 4b is checked) <small>The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.</small>	6. <input type="checkbox"/> Microfiche Computer Program (Appendix) 7. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary) a. <input type="checkbox"/> Computer Readable Copy b. <input type="checkbox"/> Paper Copy (identical to computer copy) c. <input type="checkbox"/> Statement verifying identity of above copies ACCOMPANYING APPLICATION PARTS 8. <input type="checkbox"/> Assignment Papers (cover sheet & document(s)) 9. <input type="checkbox"/> 37 CFR 3.73(b) Statement (when there is an assignee) <input type="checkbox"/> Power of Attorney 10. <input type="checkbox"/> English Translation Document (if applicable) 11. <input type="checkbox"/> Information Disclosure Statement (IDS)/PTO-1449 <input type="checkbox"/> Copies of IDS Citations 12. <input type="checkbox"/> Preliminary Amendment 13. <input checked="" type="checkbox"/> Return Receipt Postcard (MPEP 503) (Two) (should be specifically itemized) 14. <input type="checkbox"/> *Small Entity Statement(s) <input type="checkbox"/> Statement filed in prior application, Status still proper and desired 15. <input type="checkbox"/> Certified Copy of Priority Document(s) (if foreign priority is claimed) 16. <input type="checkbox"/> Other: <small>*NOTE FOR ITEMS 1 & 14 IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28)</small>
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17. If a CONTINUING APPLICATION , check appropriate box and supply the requisite information: <input type="checkbox"/> Continuation <input type="checkbox"/> Divisional <input checked="" type="checkbox"/> Continuation-in-part (CIP) of prior application No: 09/232,170 Prior Application Information: Examiner: Group/Art Unit:	
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METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF A NON-PLANT DONOR INTO A HOST PLANT IN A POSITIVE ORIENTATION

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**METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY
TRANSFECTING A NUCLEIC ACID SEQUENCE OF A NON-PLANT DONOR
INTO A HOST PLANT IN A POSITIVE ORIENTATION**

This application is a Continuation-In-Part application of U.S. Patent Application
5 Serial No. 09/232,170, filed on January 15, 1999, which is a Continuation-In-Part
application of U.S. Patent Application, Serial No. 09/008,186, filed on January 16,
1998. All the above applications are incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates generally to the field of molecular biology and
10 plant genetics. Specifically, the present invention relates to a method for determining
the presence of a trait in a host plant, and a method of changing the phenotype or
biochemistry of a host plant, by a transient expression of a nucleic acid sequence from
Monera, *Protista*, *Fungi*, or *Animalia*, in a positive sense orientation in a host plant.
This invention also relates to a method for identifying a human nucleic acid sequence
15 that silences an endogenous gene of a host plant.

BACKGROUND OF THE INVENTION

Great interest exists in launching genome projects in plants comparable to the
human genome project. Valuable and basic agricultural plants, including corn,
soybeans and rice are targets for such projects because the information obtained thereby
20 may prove very beneficial for increasing world food production and improving the
quality and value of agricultural products. The United States Congress is considering
launching a corn genome project. By helping to unravel the genetics hidden in the corn
genome, the project could aid in understanding and combating common diseases of
grain crops. It could also provide a big boost for efforts to engineer plants to improve
25 grain yields and resist drought, pests, salt, and other extreme environmental conditions.
Such advances are critical for a world population expected to double by 2050.
Currently, there are four species which provide 60% of all human food: wheat, rice,
corn, and potatoes, and the strategies for increasing the productivity of these plants is
dependent on rapid discovery of the presence of a trait in these plants, and the function
30 of unknown gene sequences in these plants. Moreover, such information could identify

genes and products encoded by genes useful for human and animal health care such as pharmaceuticals.

One strategy that has been proposed to assist in such efforts is to create a database of expressed sequence tags (ESTs) that can be used to identify expressed genes. Accumulation and analysis of expressed sequence tags (ESTs) have become an important component of genome research. EST data may be used to identify gene products and thereby accelerate gene cloning. Various sequence databases have been established in an effort to store and relate the tremendous amount of sequence information being generated by the ongoing sequencing efforts. Some have suggested sequencing 500,000 ESTs for corn and 100,000 ESTs each for rice, wheat, oats, barley, and sorghum. Efforts at sequencing the genomes of plant species will undoubtedly rely upon these computer databases to share the sequence data as it is generated.

Arabidopsis thaliana may be an attractive target discovery of a trait and for gene function discovery because a very large set of ESTs have already been produced in this organism, and these sequences tag more than 50% of the expected *Arabidopsis* genes.

Potential use of the sequence information so generated is enormous if gene function can be determined. It may become possible to engineer commercial seeds for agricultural use to convey any number of desirable traits to food and fiber crops and thereby increase agricultural production and the world food supply. Research and development of commercial seeds has so far focused primarily on traditional plant breeding, however there has been increased interest in biotechnology as it relates to plant characteristics. Knowledge of the genomes involved and the function of genes contained therein for both monocotyledonous and dicotyledonous plants is essential to realize positive effects from such technology.

The impact of genomic research in seeds is potentially far reaching. For example, gene profiling in cotton can lead to an understanding of the types of genes being expressed primarily in fiber cells. The genes or promoters derived from these genes may be important in genetic engineering of cotton fiber for increased strength or for "built-in" fiber color. In plant breeding, gene profiling coupled to physiological trait analysis can lead to the identification of predictive markers that will be increasingly important in marker assisted breeding programs. Mining the DNA sequence of a

particular crop for genes important for yield, quality, health, appearance, color, taste, etc., are applications of obvious importance for crop improvement.

Work has been conducted in the area of developing suitable vectors for expressing foreign DNA and RNA in plant hosts. Ahlquist, U.S. Patent Nos. 4,885,248
5 and 5,173,410 describes preliminary work done in devising transfer vectors which might be useful in transferring foreign genetic material into a plant host for the purpose of expression therein. All patent references cited herein are hereby incorporated by reference. Additional aspects of hybrid RNA viruses and RNA transformation vectors are described by Ahlquist *et al.* in U.S. Patent Nos. 5,466,788, 5,602,242, 5,627,060 and
10 5,500,360, all of which are incorporated herein by reference. Donson *et al.*, U.S. Patent Nos. 5,316,931, 5,589,367 and 5,866,785, incorporated herein by reference, demonstrate for the first time plant viral vectors suitable for the systemic expression of foreign genetic material in plants. Donson *et al.* describe plant viral vectors having heterologous subgenomic promoters for the systemic expression of foreign genes.
15 Carrington *et al.*, U.S. Patent 5,491,076, describe particular potyvirus vectors also useful for expressing foreign genes in plants. The expression vectors described by Carrington *et al.* are characterized by utilizing the unique ability of viral polyprotein proteases to cleave heterologous proteins from viral polyproteins. These include Potyviruses such as Tobacco Etch Virus. Additional suitable vectors are described in
20 U.S. Patent No. 5,811,653 and U.S. Patent Application Serial No. 08/324,003, both of which are incorporated herein by reference.

Construction of plant RNA viruses for the introduction and expression of non-viral foreign genes in plants has also been demonstrated by Brisson *et al.*, *Methods in Enzymology* 118:659 (1986), Guzman *et al.*, *Communications in Molecular Biology: Viral Vectors*, Cold Spring Harbor Laboratory, pp. 172-189 (1988), Dawson *et al.*,
25 *Virology* 172:285-292 (1989), Takamatsu *et al.*, *EMBO J.* 6:307-311 (1987), French *et al.*, *Science* 231:1294-1297 (1986), and Takamatsu *et al.*, *FEBS Letters* 269:73-76 (1990). However, these viral vectors have not been shown capable of systemic spread in the plant and expression of the non-viral foreign genes in the majority of plant cells in
30 the whole plant. Moreover, many of these viral vectors have not proven stable for the maintenance of non-viral foreign genes. However, the viral vectors described by Donson *et al.*, in U.S. Patent Nos. 5,316,931, 5,589,367, and 5,866,785, Turpen in U.S.

Patent No. 5,811,653, Carrington *et al.* in U.S. Patent No. 5,491,076, and in co-pending U.S. Patent Application Serial No. 08/324,003, have proven capable of infecting plant cells with foreign genetic material and systemically spreading in the plant and expressing the non-viral foreign genes contained therein in plant cells locally or
5 systemically. All patents, patent applications, and references cited in the instant application are hereby incorporated by reference.

The expression of virus-derived sense or antisense RNA in transgenic plants provides an enhanced or reduced expression of an endogenous gene. In most cases, introduction and subsequent expression of a transgene will increase (with a sense RNA)
10 or decrease (with an antisense RNA) the steady-state level of a specific gene product (Curr. Opin. Cell Biol., 7: 399-405, (1995)). There is also evidence that inhibition of endogenous genes occurs in transgenic plants containing sense RNA (Van der Krol *et al.*, Plant Cell 2(4):291-299 (1990), Napoli *et al.*, Plant Cell 2:279-289 (1990) and Fray *et al.*, Plant Mol. Biol. 22:589-602 (1993)). The posttranscriptional gene silencing
15 mechanism is typified by the highly specific degradation of both the transgene mRNA and the target RNA, which contains either the same or complementary nucleotide sequences. In cases that the silencing transgene is the same sense as the target endogenous gene or viral genomic RNA, it has been suggested that a plant-encoded RNA-dependent RNA polymerase makes a complementary strand from the transgene
20 mRNA and that the small cRNAs potentiate the degradation of the target RNA. Antisense RNA and the hypothetical cRNAs have been proposed to act by hybridizing with the target RNA to either make the hybrid a substrate for double-stranded (ds) RNases or arrest the translation of the target RNA (Baulcombe, Plant Mol. Biol. 32: 79-88 (1996)). It is also proposed that this downregulation or "co-suppression" by the
25 sense RNA might be due to the production of antisense RNA by readthrough transcription from distal promoters located on the opposite strand of the chromosomal DNA (Grierson *et al.*, Trends Biotechnol. 9:122-123 (1993)).

Waterhouse *et al* (Proc. Natl. Acad. Sci. U S A. 10: 13959-64 (1998)) prepared transgenic tobacco plants containing sense or antisense constructs. Pro[s] and Pro[a/s]
30 constructs contained the PVY nuclear inclusion Pro ORF in the sense and antisense orientations, respectively. The Pro[s]-stop construct contained the PVY Pro ORF in the sense orientation but with a stop codon three codons downstream from the initiation

codon. Waterhouse *et al* show when the genes of those constructs were transformed into plants, the plants exhibited immunity to the virus form which the transgene was derived. Smith *et al* (*Plant Cell*, 6: 1441-1453, (1994)) prepared a tobacco transgenic plant containing the potato virus Y (PVY) coat protein (CP) open reading frame, which
5 produced an mRNA rendered untranslatable by introduction of a stop codon immediately after the initiation codon. The expression of the untranslatable sense RNA inversely correlated with the virus resistance of the transgenic plant. Kumagai *et al* (*Proc. Natl. Acad. Sci. USA* 92:1679 (1995)) report that gene expression in transfected *Nicotiana benthamiana* was cytoplasmic inhibited by viral delivery of a RNA of a
10 known sequence derived from cDNA encoding tomato (*lycopersicon esculentum*) phytoene desaturase in a positive sense or an antisense orientation.

The plus sense and antisense technology can be used to develop a functional genomic screening of a plant of interest. The plus sense technology is applied in this invention to provide a method of discovering the presence of a trait in a plant and to
15 determine the function and sequence of a nucleic acid of a plant by expressing the nucleic acid sequence that has not been identified in a different host plant. GTP-binding proteins exemplify this invention. In eukaryotic cells, GTP-binding proteins function in a variety of cellular processes, including signal transduction, cytoskeletal organization, and protein transport. Low molecular weight (20-25 K Daltons) of GTP-binding
20 proteins include *ras* and its close relatives (for example, *Ran*), *rho* and its close close relatives, the *rab* family, and the ADP-ribosylation factor (ARF) family. The heterotrimeric and monomeric GTP-binding proteins that may be involved in secretion and intracellular transport are divided into two structural classes: the *rab* and the ARF families. *Ran*, a small soluble GTP-binding protein, has been shown to be essential for
25 the nuclear translocation of proteins and it is also thought to be involved in regulating cell cycle progression in mammalian and yeast cells. The cDNAs encoding GTP binding proteins have been isolated from a variety of plants including rice, barley, corn, tobacco, and *A. thaliana*. For example, Verwoert *et al.* (*Plant Molecular Biol.* 27:629-633 (1995)) report the isolation of a *Zea mays* cDNA clone encoding a GTP-binding
30 protein of the ARF family by direct genetic selection in an *E. coli fabD* mutant with a maize cDNA expression library. Regad *et al.* (*FEBS* 2:133-136 (1993)) isolated a cDNA clone encoding the ARF from a cDNA library of *Arabidopsis thaliana* cultured

cells by randomly selecting and sequencing cDNA clones. Dallmann *et al.* (*Plant Molecular Biol.* 19:847-857 (1992)) isolated two cDNAs encoding small GTP-binding proteins from leaf cDNA libraries using a PCR approach. Dallmann *et al.* prepared leaf cDNAs and use them as templates in PCR amplifications with degenerated
5 oligonucleotides corresponding to the highly conserved motifs, found in members of the *ras* superfamily, as primers. Haizel *et al.*, (*Plant J.*, 11:93-103 (1997)) isolated cDNA and genomic clones encoding Ran-like small GTP binding proteins from *Arabidopsis* cDNA and genomic libraries using a full-length tobacco *Nt Ran1* cDNA as a probe. The present invention provides advantages over the above methods in identifying
10 nucleic acid sequence encoding GTP binding proteins in that it only sequences clones that have a function and does not randomly sequence clones. The nucleic acid inserts in clones that have a function are labeled and used as probes to isolate a cDNA hybridizing to them.

For the production of some products, including products for the human health
15 industry, plants provide an optimal system because of reduced capital costs and the greater potential for large-scale production compared with microbial or animal systems. Foreign genes can be expressed in plants either by permanent insertion into the genome or by transient expression using virus-based vectors. Each approach has its own distinct advantages. Transformation for permanent expression needs to be done only once,
20 whereas each generation of plants needs to be inoculated with the transient expression vector. However, virus-based expression systems, in which the foreign mRNA is greatly amplified by virus replication, can produce very high levels of certain proteins in leaves and other tissues. Similar levels of foreign protein production in transgenic plants often are unattainable, in some cases because of gene silencing. Viral vector-
25 produced protein can be directed to specific subcellular locations, such as endomembrane, cytosol, or organelles, or it can be attached to macromolecules, such as virions, which aids purification of the protein.

The present invention provides a method for discovering the presence of a trait in a plant by expressing a nucleic acid sequence of a donor organism in a positive sense
30 orientation in a host plant. Once the presence of a trait is identified by phenotypic changes, the nucleic acid insert in the cDNA clone or in the vector is then sequenced. The present method provides a rapid method for determining the presence of a trait in a

host plant and a method for identifying a nucleic acid sequence and its function of a donor organism by screening a host plant transfected by the nucleic acid sequence of the donor organism for phenotypic or biochemical change in the host plant.

SUMMARY OF THE INVENTION

5 The present invention is directed to a method of changing the phenotype or
biochemistry of a host plant, a method of determining a change in phenotype or
biochemistry in a host plant, and a method of determining the presence of a trait in a
host plant. The method comprises the steps of expressing transiently a nucleic acid
sequence of a donor organism in a positive sense orientation in a host plant, identifying
10 changes in the host organism, and correlating the expression with the phenotypic
changes. The nucleic acid sequence does not need to be isolated, identified, or
characterized prior to transfection into the host plant. The present invention is also
directed to a method of making a functional gene profile in an organism by transiently
expressing a nucleic acid sequence library in a host plant, determining the phenotypic or
15 biochemical changes in the host plant, identifying a trait associated with the change,
identifying the donor gene associated with the trait, and identifying the homologous
host gene, if any. The present invention is also directed to a method of determining the
function of a nucleic acid sequence, including a gene, in a donor organism, by
transfecting the nucleic acid sequence into a host plant in a manner so as to affect
20 phenotypic changes in the host plant.

In one embodiment, recombinant viral nucleic acids are prepared to include the
nucleic acid insert of a donor. The recombinant viral nucleic acids infect a host plant
and produce positive sense RNAs in the cytoplasm which result in reduced expression
of endogenous cellular genes in the host plant. Once the presence of a trait is identified
25 by phenotypic changes, the function of the nucleic acid is determined. The nucleic acid
insert in a cDNA clone or in a vector is then sequenced. The nucleic acid sequence is
determined by a standard sequence analysis.

The present invention is also directed to a method of increasing yield of a grain
crop. The method comprises expressing transiently a nucleic acid sequence of a donor
30 organism in a positive sense orientation in a grain crop, for example, in the cytoplasm of
the grain crop, wherein said expressing results in stunted growth and increased seed
production of the grain crop. A preferred method comprises the steps of cloning the

nucleic acid sequence into a plant viral vector and infecting the grain crop with a recombinant viral nucleic acid comprising said nucleic acid sequence.

One aspect of the invention is a method of identifying and determining a nucleic acid sequence in a donor organism, the expression of which in a transfected host organism results in phenotypic or biochemical changes in the host organism. The method introduces the nucleic acid into the host organism by way of a viral nucleic acid such as a plant viral nucleic acid suitable to produce expression of the nucleic acid in the transfected host. One embodiment applies the principle of post-transcription gene silencing of the endogenous host gene, using positive sense RNAs. Particularly, this silencing function is useful for silencing a multigene family frequently found in plants. Another embodiment utilizes the overexpression of a plus sense RNA that results in overproduction of a protein to cause phenotypic or biochemical changes in a host plant.

Another aspect of the invention is to discover genes in a non-plant organism having the same function as that in a plant. The method starts with building a cDNA library, a genomic RNA library, or a pool of mRNA of a non-plant organism, for example, a human. Then, a recombinant viral nucleic acid comprising a nucleic acid insert derived from the library is prepared and is used to infect a host plant. The infected host plant is inspected for phenotypic changes. The recombinant viral nucleic acid that results in phenotypic changes in the host plant is identified and the sequence of the nucleic acid insert is determined by a standard method. Such nucleic acid sequence in the donor organism has substantial sequence homology as that in the host plant: the nucleic acid sequences are conserved between the non-plant organism and the plant. Once the nucleic acid is sequenced, it can be labeled and used as a probe to isolate full-length cDNAs from the donor organism or the host plant. After the amino acid sequences derived from the cDNAs of the donor organism and the plant are compared, the plant cDNA sequence can be changed so that it encodes the same amino acid sequence as the cDNA of the donor organism encodes. This invention provides a rapid means for elucidating the function and sequence of nucleic acids of a donor organism; such rapidly expanding information can be subsequently utilized in the field of genomics.

In one embodiment, a nucleic acid is introduced into a plant host wherein the plant host may be a monocotyledonous or dicotyledonous plant, plant tissue or plant

cell. Preferably, the nucleic acid is introduced by way of a recombinant plant viral nucleic acid. Preferred recombinant plant viral nucleic acids useful in the present invention comprise a native plant viral subgenomic promoter, a plant viral coat protein coding sequence, and at least one non-native nucleic acid sequence. Some viral vectors
5 used in accordance with the present invention may be encapsidated by the coat proteins encoded by the recombinant plant virus. Recombinant plant viral nucleic acids or recombinant plant viruses are used to infect a plant host. The recombinant plant viral nucleic acid is capable of replication in the host, localized or systemic spread in the host, and transcription or expression of the non-native nucleic acid in the host to
10 produce a phenotypic or biochemical change. Any suitable vector constructs useful to produce localized or systemic expression of nucleic acids in host plants are within the scope of the present invention.

BRIEF DESCRIPTION OF THE FIGURES

- FIG. 1 depicts the vector TT01/PSY+.
- 15 FIG. 2 depicts the vector TT01A/PDS+.
- FIG. 3 depicts the vector TT01A/CaCCS+.
- FIG. 4 depicts the plasmid KS + TVCVK #23.
- FIG. 5 depicts the plasmid TTU51 CTP CrtB.
- FIG. 6 shows the plasmid TT0SA1 APE ZZA1.
- 20 FIG. 7 depicts the plasmid pBS 735.
- FIG. 8 depicts the plasmid pBS 740.
- FIG. 9 depicts the plasmid TTU51A QSE0 #3.
- FIG. 10 depicts the plasmid pBS 723.
- FIG. 11 depicts the plasmid pBS 731.
- 25 FIG. 12 depicts the plasmid pBS 740 AT #2441 (ATCC No: PTA-332).
- FIG. 13 shows the nucleotide sequence of 740 AT #2441.
- FIG. 14 shows the nucleotide sequence alignment of 740 AT #2441 and AF017991, a *A. thaliana* salt stress inducible small GTP binding protein RAN1.
- FIG. 15 shows the nucleotide sequence alignment of 740 AT #2441 and L16787,
30 a *N. tabacum* small GTP-binding protein..
- FIG. 16 shows the amino acid comparison of 740 AT #2441 to a tobacco RAN-B1 GTP binding protein.

FIG. 17 shows the pBS 740 AT #1191 plasmid map.

FIG. 18 shows the nucleotide and amino acid sequence of 740 AT #1191.

FIG. 19 depicts the plasmid pBS 740 AT #855 (ATCC No: PTA-325).

FIG. 20 shows the nucleotide sequence alignment of 740 AT #855 to *A. thaliana*
5 HAT7 homeobox protein ORF (U09340).

FIG. 21 depicts the plasmid 740 AT #909 (ATCC No: PTA-330).

FIG. 22 shows the nucleotide sequence alignment of 740 AT #909 insert and *H.*
sapiens S556985 ribosomal protein L19 derived from a human breast cancer cell line,
MCF-7.

10 FIG. 23 shows the amino acid sequence alignment of 740 AT #909 to human
P14418 60S ribosomal protein L19.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to a method of changing the phenotype or
biochemistry of a host plant, a method of determining a change in phenotype or
15 biochemistry in an organism, a method of determining the presence of a trait in an
organism, and a method of determining the function and sequence of a nucleic acid in a
non-plant organism. The methods comprise the steps of a transient expression of a
nucleic acid sequence of a donor organism in a positive sense orientation in a host
organism; identifying changes in the host organism; and correlating the expression and
20 the changes. The presence of a trait is identified either in the infected host organism or
in an uninfected host organism. A preferred host organism includes a plant, a plant
tissue or a plant cell. In one preferred embodiment, the method comprising the steps of
(a) preparing a library of cDNA, genomic DNA, or a mRNA pool of a donor organism,
(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived
25 from the library, (c) infecting each host plant with one of the recombinant viral nucleic
acids, (d) growing the infected host plant, and (e) determining changes in the host plant.

The invention is directed to a method of compiling a positive sense functional
gene profile of an organism. The method comprises (a) preparing a vector library of
DNA or RNA sequences from a donor organism, each sequence being in a positive
30 sense orientation; (b) infecting a plant host with a vector; (c) transiently expressing the
donor DNA or RNA sequence in the growing plant host; (d) determining one or more
phenotypic or biochemical changes in the plant host, if any; (e) identifying an associated

trait where a phenotypic or biochemical change occurs; (f) identifying a donor gene associated with the trait; (g) identifying a plant host gene, if any, associated with the trait; and (h) repeating steps (b) – (g) until an antisense functional gene profile of the plant host and/or of the donor organism is compiled.

5 The present method has the advantages that the nucleic acid sequence does not need to be identified, known, or characterized prior to infecting a host plant with a recombinant viral nucleic acid comprising the nucleic acid sequence. Once changes in the host plant is observed, the nucleic acid sequence can be determined by further identifying the recombinant viral nucleic acid that results in changes in the host, and
10 analyzing the sequence of the nucleic acid insert in the recombinant viral nucleic acid that results in changes in the host.

 The present invention provides a method of infecting a host plant by a recombinant viral nucleic acid which contains one or more non-native nucleic acid sequences, or by a recombinant virus containing a recombinant viral nucleic acid. The
15 non-native nucleic acids are subsequently transcribed or expressed in the infected host plant in a plus sense orientation, which results in (a) overexpressing a new protein, (b) inhibiting an endogeneous gene expression, or (c) enhancing an endogeneous gene expression, in the host organism. The inhibition of an endogeneous gene may result from co-suppression by the production of antisense RNA by readthrough transcription
20 from distal promoters located on the opposite strand of the chromosomal DNA. The inhibition may also result from the expression of a partial cDNA gene, which sometimes lacks of a start codon or has a stop codon close to the start codon. The inhibition may also result from the expression of a nucleic acid sequence encoding a 3'- or 5'- untranslated region similar or identical to that of the endogeneous gene. The expression
25 of the non-native nucleic acid sequences result in changing phenotypic traits in the host organism, affecting biochemical pathways within the organism, or affecting endogenous gene expression within the organism.

 In one embodiment, a nucleic acid is introduced into a plant host by way of a recombinant viral nucleic acid. Such recombinant viral nucleic acids are stable for the
30 maintenance and transcription or expression of non-native nucleic acid sequences and are capable of systemically transcribing or expressing such non-native sequences in the plant host. Preferred recombinant plant viral nucleic acids useful in the present

invention comprise a native plant viral subgenomic promoter, a plant viral coat protein coding sequence, and at least one non-native nucleic acid sequence.

In a second embodiment, plant viral nucleic acid sequences are characterized by the deletion of a native coat protein coding sequence. The plant viral nucleic acid sequence comprises a non-native plant viral coat protein coding sequence and a non-native promoter, preferably the subgenomic promoter of the non-native coat protein coding sequence. Such plant viral nucleic acid sequence is capable of expressing in a plant host, packaging the recombinant plant viral nucleic acid, and ensuring a systemic infection of the host by the recombinant plant viral nucleic acid. The recombinant plant viral nucleic acid may contain one or more additional native or non-native subgenomic promoters. Each non-native subgenomic promoter is capable of transcribing or expressing adjacent genes or nucleic acid sequences in the plant host and incapable of recombination with each other and with native subgenomic promoters. One or more non-native nucleic acids may be inserted adjacent to the native plant viral subgenomic promoter or the native and non-native plant viral subgenomic promoters if more than one nucleic acid sequence is included. Moreover, two or more heterologous non-native subgenomic promoters may be used. The non-native nucleic acid sequences may be transcribed or expressed in the host plant under the control of the subgenomic promoter to produce the products of the nucleic acids of interest.

In a third embodiment, plant recombinant viral nucleic acids comprise a native coat protein coding sequence instead of a non-native coat protein coding sequence, placed adjacent one of the non-native coat protein subgenomic promoters.

In a fourth embodiment, plant recombinant viral nucleic acids comprise a native coat protein gene adjacent its native subgenomic promoter, one or more non-native subgenomic promoters, and at least one non-native nucleic acid sequence. The native plant viral subgenomic promoter initiates transcription of the plant viral coat protein sequence. The non-native subgenomic promoters are capable of transcribing or expressing adjacent genes in a plant host and are incapable of recombination with each other and with native subgenomic promoters. Non-native nucleic acid sequences may be inserted adjacent the non-native subgenomic plant viral promoters such that the sequences are transcribed or expressed in the host plant under control of the subgenomic promoters to produce a product of the non-native nucleic acid. Alternatively, the native

coat protein coding sequence may be replaced by a non-native coat protein coding sequence.

The viral vectors used in accordance with the present invention may be encapsidated by the coat proteins encoded by the recombinant plant virus. The
5 recombinant plant viral nucleic acid or recombinant plant virus is used to infect a host plant. The recombinant plant viral nucleic acid is capable of replication in the host, localized or systemic spread in the host, and transcription or expression of the non-native nucleic acid in the host to affect a phenotypic or biochemical change in the host.

In one embodiment, recombinant plant viruses are used which encode for the
10 expression of a fusion between a plant viral coat protein and the amino acid product of the nucleic acid of interest. Such a recombinant plant virus provides for high level expression of a nucleic acid of interest. The location or locations where the viral coat protein is joined to the amino acid product of the nucleic acid of interest may be referred to as the fusion joint. A given product of such a construct may have one or more fusion
15 joints. The fusion joint may be located at the carboxyl terminus of the viral coat protein or the fusion joint may be located at the amino terminus of the coat protein portion of the construct. In instances where the nucleic acid of interest is located internal with respect to the 5' and 3' residues of the nucleic acid sequence encoding for the viral coat protein, there are two fusion joints. That is, the nucleic acid of interest may be located
20 5', 3', upstream, downstream or within the coat protein. In some embodiments of such recombinant plant viruses, a "leaky" start or stop codon may occur at a fusion joint which sometimes does not result in translational termination. A more detailed description of some recombinant plant viruses according to this embodiment of the invention may be found in co-pending U.S. Patent Application Serial No. 08/324,003
25 the disclosure of which is incorporated herein by reference.

The present invention is not intended to be limited to any particular viral constructs, but rather to include all operable constructs. Specifically, those skilled in the art may choose to transfer DNA or RNA of any size up to and including an entire
30 genome in an organism into a host plant in order to determine the presence of a trait in the plant. Those skilled in the art will understand that the recited embodiments are representative only. All operable constructs useful to produce localized or systemic expression of nucleic acids in a plant are within the scope of the present invention.

5 The chimeric genes and vectors and recombinant plant viral nucleic acids used
in this invention are constructed using techniques well known in the art. Suitable
techniques have been described in Sambrook *et al.* (2nd ed.), Cold Spring Harbor
Laboratory, Cold Spring Harbor (1982, 1989); *Methods in Enzymol.* (Vols. 68, 100,
101, 118, and 152-155) (1979, 1983, 1986 and 1987); and *DNA Cloning*, D.M. Glover,
10 Ed., IRL Press, Oxford (1985). Medium compositions have been described by Miller,
J., *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory, New York
(1972), as well as the references previously identified, all of which are incorporated
herein by reference. DNA manipulations and enzyme treatments are carried out in
10 accordance with manufacturers' recommended procedures in making such constructs.

15 The first step in producing recombinant plant viral nucleic acids is to modify the
nucleotide sequences of the plant viral nucleotide sequence by known conventional
techniques such that one or more non-native subgenomic promoters are inserted into the
plant viral nucleic acid without destroying the biological function of the plant viral
nucleic acid. The subgenomic promoters are capable of transcribing or expressing
adjacent nucleic acid sequences in a plant host infected by the recombination plant viral
nucleic acid or recombinant plant virus. The native coat protein coding sequence may
be deleted in some embodiments, placed under the control of a non-native subgenomic
promoter in other embodiments, or retained in a further embodiment. If it is deleted or
20 otherwise inactivated, a non-native coat protein gene is inserted under control of one of
the non-native subgenomic promoters, or optionally under control of the native coat
protein gene subgenomic promoter. The non-native coat protein is capable of
encapsidating the recombinant plant viral nucleic acid to produce a recombinant plant
virus. Thus, the recombinant plant viral nucleic acid contains a coat protein coding
25 sequence, which may be native or a nonnative coat protein coding sequence, under
control of one of the native or non-native subgenomic promoters. The coat protein is
involved in the systemic infection of the plant host.

30 Viruses suitable for use according to the methods of the present invention
include viruses from the tobamovirus group such as Tobacco Mosaic virus (TMV),
Ribgrass Mosaic Virus (RGM), Cowpea Mosaic virus (CMV), Alfalfa Mosaic virus
(AMV), Cucumber Green Mottle Mosaic virus watermelon strain (CGMMV-W) and
Oat Mosaic virus (OMV) and viruses from the brome mosaic virus group such as Brome

Mosaic virus (BMV), broad bean mottle virus and cowpea chlorotic mottle virus. Additional suitable viruses include Rice Necrosis virus (RNV), and geminiviruses such as Tomato Golden Mosaic virus (TGMV), Cassava Latent virus (CLV) and Maize Streak virus (MSV). Each of these groups of suitable viruses is characterized below.

- 5 However, the invention should not be construed as limited to using these particular viruses, but rather the present invention is contemplated to include all plant viruses at a minimum.

TOBAMOVIRUS GROUP

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The tobacco mosaic virus (TMV) is of particular interest to the instant invention because of its ability to express genes at high levels in plants. TMV is a member of the tobamovirus group. The TMV virion is a tubular filament, and comprises coat protein sub-units arranged in a single right-handed helix with the single-stranded RNA intercalated between the turns of the helix. TMV infects tobacco as well as other plants. TMV virions are 300 nm x 18 nm tubes with a 4 nm-diameter hollow canal, and consist of 2140 units of a single structural protein helically wound around a single RNA molecule. The genome is a 6395 base plus-sense RNA. The 5'-end is capped and the 3'-end contains a series of pseudoknots and a tRNA-like structure that will specifically accept histidine. The genomic RNA functions as mRNA for the production of proteins involved in viral replication: a 126-kDa protein that initiates 68 nucleotides from the 5'-terminus, and a 183-kDa protein synthesized by readthrough of an amber termination codon approximately 10% of the time. Only the 183-kDa and 126-kDa viral proteins are required for the TMV replication in trans. (Ogawa *et al.*, Virology 185:580-584 (1991)). Additional proteins are translated from subgenomic size mRNA produced during replication (Dawson, *Adv. Virus Res.*, 38:307-342 (1990)). The 30-kDa protein is required for cell-to-cell movement; the 17.5-kDa capsid protein is the single viral structural protein. The function of the predicted 54-kDa protein is unknown.

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TMV assembly apparently occurs in plant cell cytoplasm, although it has been suggested that some TMV assembly may occur in chloroplasts since transcripts of ctDNA have been detected in purified TMV virions. Initiation of TMV assembly occurs by interaction between ring-shaped aggregates ("discs") of coat protein (each disc consisting of two layers of 17 subunits) and a unique internal nucleation site in the RNA; a hairpin region about 900 nucleotides from the 3'-end in the common strain of

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TMV. Any RNA, including subgenomic RNAs containing this site, may be packaged into virions. The discs apparently assume a helical form on interaction with the RNA, and assembly (elongation) then proceeds in both directions (but much more rapidly in the 3' - to 5' - direction from the nucleation site).

5 Another member of the Tobamoviruses, the Cucumber Green Mottle Mosaic virus watermelon strain (CGMMV-W) is related to the cucumber virus. Nozu *et al.*, *Virology* 45:577 (1971). The coat protein of CGMMV-W interacts with RNA of both TMV and CGMMV to assemble viral particles *in vitro*. Kurisu *et al.*, *Virology* 70:214 (1976).

10 Several strains of the tobamovirus group are divided into two subgroups, on the basis of the location of the assembly of origin. Subgroup I, which includes the vulgare, OM, and tomato strain, has an origin of assembly about 800-1000 nucleotides from the 3'-end of the RNA genome, and outside the coat protein cistron. Lebeurier *et al.*, *Proc. Natl. Acad. Sci. USA* 74:149 (1977); and Fukuda *et al.*, *Virology* 101:493 (1980).

15 Subgroup II, which includes CGMMV-W and cowpea strain (Cc) has an origin of assembly about 300-500 nucleotides from the 3'-end of the RNA genome and within the coat-protein cistron. The coat protein cistron of CGMMV-W is located at nucleotides 176-661 from the 3'-end. The 3' noncoding region is 175 nucleotides long. The origin of assembly is positioned within the coat protein cistron. Meshi *et al.*, *Virology* 127:54
20 (1983).

BROME MOSAIC VIRUS GROUP

Brome Mosaic virus (BMV) is a member of a group of tripartite, single-stranded, RNA-containing plant viruses commonly referred to as the bromoviruses. Each member of the bromoviruses infects a narrow range of plants. Mechanical
25 transmission of bromoviruses occurs readily, and some members are transmitted by beetles. In addition to BV, other bromoviruses include broad bean mottle virus and cowpea chlorotic mottle virus.

Typically, a bromovirus virion is icosahedral, with a diameter of about 26 μ m, containing a single species of coat protein. The bromovirus genome has three
30 molecules of linear, positive-sense, single-stranded RNA, and the coat protein mRNA is also encapsidated. The RNAs each have a capped 5'-end, and a tRNA-like structure

(which accepts tyrosine) at the 3'-end. Virus assembly occurs in the cytoplasm. The complete nucleotide sequence of BMV has been identified and characterized as described by Ahlquist *et al.*, *J. Mol. Biol.* 153:23 (1981).

RICE NECROSIS VIRUS

5 Rice Necrosis virus is a member of the Potato Virus Y Group or Potyviruses. The Rice Necrosis virion is a flexuous filament comprising one type of coat protein (molecular weight about 32,000 to about 36,000) and one molecule of linear positive-sense single-stranded RNA. The Rice Necrosis virus is transmitted by *Polymyxa oraminis* (a eukaryotic intracellular parasite found in plants, algae and fungi).

GEMINIVIRUSES

10 Geminiviruses are a group of small, single-stranded DNA-containing plant viruses with virions of unique morphology. Each virion consists of a pair of isometric particles (incomplete icosahedral), composed of a single type of protein (with a molecular weight of about $2.7-3.4 \times 10^4$). Each geminivirus virion contains one
15 molecule of circular, positive-sense, single-stranded DNA. In some geminiviruses (*i.e.*, Cassava latent virus and bean golden mosaic virus) the genome appears to be bipartite, containing two single-stranded DNA molecules.

POTYVIRUSES

20 Potyviruses are a group of plant viruses which produce polyprotein. A particularly preferred potyvirus is tobacco etch virus (TEV). TEV is a well characterized potyvirus and contains a positive-strand RNA genome of 9.5 kilobases encoding for a single, large polyprotein that is processed by three virus-specific proteinases. The nuclear inclusion protein "a" proteinase is involved in the maturation of several replication-associated proteins and capsid protein. The helper component-
25 proteinase (HC-Pro) and 35-kDa proteinase both catalyze cleavage only at their respective C-termini. The proteolytic domain in each of these proteins is located near the C-terminus. The 35-kDa proteinase and HC-Pro derive from the N-terminal region of the TEV polyprotein.

30 The nucleic acid of any suitable virus can be utilized to prepare a recombinant viral nucleic acid for use in the present invention, and the foregoing are only exemplary

of such suitable viruses. The nucleotide sequence of the virus can be modified, using conventional techniques, by insertion of one or more subgenomic promoters into the viral nucleic acid. The subgenomic promoters are capable of functioning in a specific host. For example, if the host is a tobacco plant, TMV, TEV, or other viruses
5 containing suitable subgenomic promoter may be utilized. The inserted subgenomic promoters should be compatible with the viral nucleic acid and capable of directing transcription or expression of adjacent nucleic acid sequences in tobacco.

The native or non-native coat protein gene is included in the recombinant nucleic acid. When non-native nucleic acid is utilized, it may be positioned adjacent its
10 natural subgenomic promoter or adjacent one of the other available subgenomic promoters. The non-native coat protein, as is the case for the native coat protein, is capable of encapsidating the recombinant viral nucleic acid and providing for systemic spread of the recombinant viral nucleic acid in a host organism. The coat protein is selected to provide a systemic infection in the host. For example, the TMV-O coat
15 protein provides systemic infection in *N. benthamiana*, whereas TMV-U1 coat protein provides systemic infection in *N. tabacum*

The recombinant viral nucleic acid is prepared by cloning a viral nucleic acid. If the viral nucleic acid is DNA, it can be cloned directly into a suitable vector using conventional techniques. One technique is to attach an origin of replication to the viral
20 DNA which is compatible with the cell to be transfected. If the viral nucleic acid is RNA, a full-length DNA copy of the viral genome is first prepared by well-known procedures. For example, the viral RNA is transcribed into DNA using reverse transcriptase to produce subgenomic DNA pieces, and a double-stranded DNA made using DNA polymerases. The cDNA is then cloned into appropriate vectors and cloned
25 into a cell to be transfected. Alternatively, the cDNA is ligated into the vector and is directly transcribed into infectious RNA *in vitro*, the infectious RNA is then inoculated onto the host. The cDNA pieces are mapped and combined in a proper sequence to produce a full-length DNA copy of the viral RNA genome, if necessary. DNA
30 sequences for the subgenomic promoters, with or without a coat protein gene, are then inserted into the nucleic acid at non-essential sites, according to the particular embodiment of the invention utilized. Non-essential sites are those that do not affect the biological properties of the viral nucleic acids. Since the RNA genome is the

infective agent, the cDNA is positioned adjacent a suitable promoter so that the RNA is produced in the production cell. The RNA can be capped by the addition of a nucleotide using conventional techniques (Dawson *et al.*, *Proc. Natl. Acad. Sci. USA*, 83:1832 (1986)), between the transcription start site of the promoter and the start of the cDNA of a viral nucleic acid. One or more nucleotides may be added. In a preferred embodiment of the present invention, the inserted nucleotide sequence contains a G at the 5'-end. In one embodiment, the inserted nucleotide sequence is GNN, GTN, or their multiples, (GNN)*x* or (GTN)*x*. The capped RNA can be packaged in vitro with added coat protein from TMV to make assembled virions. These assembled virions can then be used to inoculate plants or plant tissues.

Alternatively, an uncapped RNA may be employed in the embodiments of the present invention. Contrary to the practiced art in scientific literature and in an issued patent (Ahlquist *et al.*, U.S. Patent No. 5,466,788), uncapped transcripts for virus expression vectors are infective on both plants and in plant cells. Capping is not a prerequisite for establishing an infection of a virus expression vector in plants, although capping increases the efficiency of infection.

One feature of the recombinant plant viral nucleic acids useful in the present invention is that they further comprise one or more non-native nucleic acid sequences capable of being transcribed in a host plant. These nucleic acid sequences may be native nucleic acid sequences that occur in a host plant. Preferably, these nucleic acid sequences are non-native nucleic acid sequences that do not normally occur in a host plant. These nucleic acid sequences are derived from a donor organism, which preferably belongs to a non-plant kingdom. Non-plant kingdoms include kingdom *Monera*, Kingdom *Protista*, Kingdom *Fungi* and Kingdom *Animalia*. Kingdom *Monera* includes subkingdom *Archaeobacteriobionta* (archaeobacteria): division *Archaeobacteriophyta* (methane, salt and sulfolobus bacteria); subkingdom *Eubacteriobionta* (true bacteria): division *Eubacteriophyta*; subkingdom *Viroids*; and subkingdom *Viruses*. Kingdom *Protista* includes subkingdom *Phycobionta*: division *Xanthophyta* 275 (yellow-green algae), division *Chrysophyta* 400 (golden-brown algae), division *Dinophyta* (Pyrrhophyta) 1,000 (dinoflagellates), division *Bacillariophyta* 5,500 (diatoms), division *Cryptophyta* 74 (cryptophytes), division *Haptophyta* 250 (haptonema organisms), division *Euglenophyta* 550 (euglenoids), division *Chlorophyta*,

class *Chlorophyceae* 10,000 (green algae), class *Charophyceae* 200 (stoneworts),
division *Phaeophyta* 900 (brown algae), and division *Rhodophyta* 2,500 (red algae);
subkingdom *Mastigobionta* 960: division *Chytridiomycota* 750 (chytrids), and division
Oomycota (water molds) 475; subkingdom *Myxobionta* 320: division *Acrasiomycota*
5 (cellular slime molds) 21, and division *Myxomycota* 500 (true slime molds). Kingdom
Fungi includes division *Zygomycota* 570 (coenocytic fungi): subdivision
Zygomycotina; and division *Eumycota* 350 (septate fungi): subdivision *Ascomycotina*
56,000 (cup fungi), subdivision *Basidiomycotina* 25,000 (club fungi), subdivision
Deuteromycotina 22,000 (imperfect fungi), and subdivision *Lichenes* 13,500. A
10 preferred donor organism is human. Host plants are those capable of being infected by
an infectious RNA or a virus containing a recombinant viral nucleic acid. Host plants
include plants of commercial interest, such as food crops, seed crops, oil crops,
ornamental crops and forestry crops. For example, wheat, rice, corn, potatoes, barley,
tobaccos, soybean canola, maize, oilseed rape, *Arabidopsis*, and *Nicotiana*, can be
15 selected as a host plant. Preferred host plants include *Nicotiana*, preferably, *Nicotiana*
benthamiana, or *Nicotiana cleavlandii*. Plants are grown from seed in a mixture of
“Peat-Lite Mix™ (Speedling, Inc. Sun City, FL) and Nutricote™ controlled release
fertilizer 14-14-14 (Chiss-Asahi Fertilizer Co., Tokyo, Japan). Plants are grown in a
controlled environment provided 16 hours of light and 8 hours of darkness. Sylvania
20 “Gro-Lux/Aquarium” wide spectrum 40 watt fluorescent grow lights (Osram Sylvania
Products, Inc. Danvers, MA.) are used. Temperatures are kept at around 80° F during
light hours and 70° F during dark hours. Humidity is between 60 and 85%.

To prepare a DNA insert comprising a nucleic acid sequence of a donor
organism, the first step is to construct a cDNA library, a genomic DNA library, or a
25 pool of RNA of the donor organism. Full-length cDNAs or genomic DNAs can be
obtained from public or private repositories. For example, cDNA and genomic libraries
from bovine, chicken, dog, drosophila, fish, frog, human, mouse, porcine, rabbit, rat,
and yeast; and retroviral libraries can be obtained from clontech (Palo Alto, CA).
Alternatively, cDNA library can be prepared from a field sample by methods known to
30 a person of ordinary skill, for example, isolating mRNAs and transcribing mRNAs into
cDNAs by reverse transcriptase (see, e.g., Sambrook *et al.*, *Molecular Cloning: A*
Laboratory Manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989), or

Current Protocols in Molecular Biology, F. Ausubel *et al.*, ed. Greene Publishing and Wiley-Interscience, New York (1987)). Genomic DNAs represented in BAC (bacterial artificial chromosome), YAC (yeast artificial chromosome), or TAC (transformation-competent artificial chromosome, Lin *et al.*, *Proc. Natl. Acad. Sci. USA*, 96:6535-6540 (1999)) libraries can be obtained from public or private repositories. Alternatively, a pool of genes, which are overexpressed in a tumor cell line compared with a normal cell line, can be prepared or obtained from public or private repositories. Zhang *et al* (*Science*, 276: 1268-1272 (1997)) report that using a method of serial analysis of gene expression (SAGE) (Velculescu *et al*, *Cell*, 88:243 (1997)), 500 transcripts that were expressed at significantly different levels in normal and neoplastic cells were identified. The expression of DNAs that overexpresses in a tumor cell line in a host plant may cause changes in the host plant, thus a pool of such DNAs is another source for DNA inserts for this invention. The BAC/YAC/TAC DNAs, DNAs or cDNAs can be mechanically size-fractionated or digested by an enzyme to smaller fragments. The fragments are ligated to adapters with cohesive ends, and shotgun-cloned into recombinant viral nucleic acid vectors. Alternatively, the fragments can be blunt-end ligated into recombinant viral nucleic acid vectors. Recombinant plant viral nucleic acids containing a nucleic acid sequence derived from the cDNA library or genomic DNA library is then constructed using conventional techniques. The recombinant viral nucleic acid vectors produced comprise the nucleic acid insert derived from the donor plant. The nucleic acid sequence of the recombinant viral nucleic acid is transcribed as RNA in a host plant; the RNA is capable of regulating the expression of a phenotypic trait by a positive sense mechanism. The nucleic acid sequence may also regulate the expression of more than one phenotypic trait. Nucleic acid sequences from *Monera*, *Protista*, *Fungi*, and *Animalia* may be used to assemble the DNA libraries. This method may thus be used to discover useful dominant gene phenotypes from DNA libraries through the gene expression in a host plant.

An alternative when creating the recombinant plant viral nucleic acid is to prepare more than one nucleic acid (*i.e.*, to prepare the nucleic acids necessary for a multipartite viral vector construct). In this case, each nucleic acid would require its own origin of assembly. Each nucleic acid could be prepared to contain a subgenomic promoter and a non-native nucleic acid.

In some embodiments of the instant invention, methods to increase the representation of gene sequences in virus expression libraries may also be achieved by bypassing the genetic bottleneck of propagation in bacterial cells. For example, cell-free methods may be used to assemble sequence libraries or individual arrayed sequences into virus expression vectors and reconstruct an infectious virus, such that the final ligation product can be transcribed and the resulting RNA can be used for host organism inoculation/infection. A more detailed discussion is presented in a co-pending and co-owned U.S. Patent Application No. ____ (Padgett et al., Docket No. 08010137US03, filed July 21, 1999), which is incorporated herein by reference.

- 10 The host plant can be infected with a recombinant viral nucleic acid or a recombinant plant virus by conventional techniques. Suitable techniques include, but are not limited to, leaf abrasion, abrasion in solution, high velocity water spray, and other injury of a host as well as imbibing host seeds with water containing the recombinant viral RNA or recombinant plant virus. More specifically, suitable
- 15 techniques include:
- (a) Hand Inoculations. Hand inoculations are performed using a neutral pH, low molarity phosphate buffer, with the addition of celite or carborundum (usually about 1%). One to four drops of the preparation is put onto the upper surface of a leaf and gently rubbed.
 - 20 (b) Mechanized Inoculations of Plant Beds. Plant bed inoculations are performed by spraying (gas-propelled) the vector solution into a tractor-driven mower while cutting the leaves. Alternatively, the plant bed is mowed and the vector solution sprayed immediately onto the cut leaves.
 - (c) Vacuum Infiltration. Inoculations may be accomplished by subjecting a host organism to a substantially vacuum pressure environment in order to facilitate infection.
 - 25 (d) High Speed Robotics Inoculation. Especially applicable when the organism is a plant, individual organisms may be grown in mass array such as in microtiter plates. Machinery such as robotics may then be used to transfer the nucleic acid of interest.
 - 30 (e) High Pressure Spray of Single Leaves. Single plant inoculations can also be performed by spraying the leaves with a narrow, directed spray (50 psi, 6-12

inches from the leaf) containing approximately 1% carborundum in the buffered vector solution.

- (f) Ballistics (High Pressure Gun) Inoculation. Single plant inoculations can also be performed by particle bombardment. A ballistics particle delivery system (BioRad Laboratories, Hercules, (A) can be used to transfect plants such as *N. benthamiana* as described previously (Nagar *et al.*, *Plant Cell*, 7:705-719 (1995)).

An alternative method for introducing a recombinant plant viral nucleic acid into a plant host is a technique known as agroinfection or *Agrobacterium*-mediated transformation (sometimes called Agro-infection) as described by Grimsley *et al.*, *Nature* 325:177 (1987), and Turpen *et al* (*J. Virol. Methods*, 42:227-240 (1993)). This technique makes use of a common feature of *Agrobacterium* which colonizes plants by transferring a portion of their DNA (the T-DNA) into a host cell, where it becomes integrated into nuclear DNA. The T-DNA is defined by border sequences which are 25 base pairs long, and any DNA between these border sequences is transferred to the plant cells as well. The insertion of a recombinant plant viral nucleic acid between the T-DNA border sequences results in transfer of the recombinant plant viral nucleic acid to the plant cells, where the recombinant plant viral nucleic acid is replicated, and then spreads systemically through the plant. Agro-infection has been accomplished with potato spindle tuber viroid (PSTV) (Gardner *et al.*, *Plant Mol. Biol.* 6:221 (1986); CaV (Grimsley *et al.*, *Proc. Natl. Acad. Sci. USA* 83:3282 (1986)); MSV (Grimsley *et al.*, *Nature* 325:177 (1987)), and Lazarowitz, S., *Nucl. Acids Res.* 16:229 (1988)) digitaria streak virus (Donson *et al.*, *Virology* 162:248 (1988)), wheat dwarf virus (Hayes *et al.*, *J. Gen. Virol.* 69:891 (1988)) and tomato golden mosaic virus (TGMV) (Elmer *et al.*, *Plant Mol. Biol.* 10:225 (1988) and Gardiner *et al.*, *EMBO J.* 7:899 (1988)). Therefore, agro-infection of a susceptible plant could be accomplished with a virion containing a recombinant plant viral nucleic acid based on the nucleotide sequence of any of the above viruses. Particle bombardment or electroporation or any other methods known in the art may also be used.

- 30 Infection may also be attained by placing a selected nucleic acid sequence into an organism such as *E. coli*, or yeast, either integrated into the genome of such organism or not, and then applying the organism to the surface of the host organism. Such a

mechanism may thereby produce secondary transfer of the selected nucleic acid sequence into a host organism. This is a particularly practical embodiment when the host organism is a plant. Likewise, infection may be attained by first packaging a selected nucleic acid sequence in a pseudovirus. Such a method is described in WO
5 94/10329, the teachings of which are incorporated herein by reference. Though the teachings of this reference may be specific for bacteria, those of skill in the art will readily appreciate that the same procedures could easily be adapted to other organisms.

After a host is infected with a recombinant viral nucleic acid comprising a nucleic acid insert derived from a cDNA library or a genomic library, one or more
10 biochemical or phenotypic changes in a host plant is determined. The biochemical or phenotypic changes in the infected host plant is correlated to the biochemistry or phenotype of a host plant that is uninfected. Optionally, the biochemical or phenotypic changes in the infected host plant is further correlated to a host plant that is infected with a viral vector that contains a control nucleic acid of a known sequence in a positive
15 sense orientation; the control nucleic acid has similar size but is different in sequence from the nucleic acid insert derived from the library. For example, if the nucleic acid insert derived from the library is identified as encoding a GTP binding protein in a positive sense orientation, a nucleic acid derived from a gene encoding green fluorescent protein can be used as a control nucleic acid. Green fluorescent protein is
20 known not to have the same effect as the GTP binding protein when expressed in plants.

Those of skill in the art will readily understand that there are many methods to determine phenotypic or biochemical change in a plant and to determine the function of a nucleic acid, once the nucleic acid is localized or systemically expressed in a host plant.
25 In a preferred embodiment, the phenotypic or biochemical trait may be determined by observing phenotypic changes in a host by methods including visual, morphological, macroscopic or microscopic analysis. For example, growth change such as stunting, hyperbranching, and necrosis; structure change such as vein banding, ring spot, etching; color change such as bleaching, chlorosis, or other color; and other changes such as
30 marginal, mottled, patterning, punctate, and reticulate are easily detected. In another embodiment, the phenotypic or biochemical trait may be determined by complementation analysis, that is, by observing the endogenous gene or genes whose

function is replaced or augmented by introducing the nucleic acid of interest. A discussion of such phenomenon is provided by Napoli *et al.*, *The Plant Cell* 2:279-289 (1990). In a third embodiment, the phenotypic or biochemical trait may be determined by analyzing the biochemical alterations in the accumulation of substrates or products
5 from enzymatic reactions according to any means known by those skilled in the art. In a fourth embodiment, the phenotypic or biochemical trait may be determined by observing any changes in biochemical pathways which may be modified in a host plant as a result of expression of the nucleic acid. In a fifth embodiment, the phenotypic or biochemical trait may be determined utilizing techniques known by those skilled in the
10 art to observe inhibition of endogenous gene expression in the cytoplasm of cells as a result of expression of the nucleic acid. In a sixth embodiment, the phenotypic or biochemical trait may be determined utilizing techniques known by those skilled in the art to observe changes in the RNA or protein profile as a result of expression of the nucleic acid. In a seventh embodiment, the phenotypic or biochemical trait may be
15 determined by selection of organisms such as plants capable of growing or maintaining viability in the presence of noxious or toxic substances, such as, for example herbicides and pharmaceutical ingredients.

Phenotypic traits in plant cells, which may be observed microscopically, macroscopically or by other methods, include improved tolerance to herbicides,
20 improved tolerance to extremes of heat or cold, drought, salinity or osmotic stress; improved resistance to pests (insects, nematodes or arachnids) or diseases (fungal, bacterial or viral), production of enzymes or secondary metabolites; male or female sterility; dwarfness; early maturity; improved yield, vigor, heterosis, nutritional qualities, flavor or processing properties, and the like. Other examples include the
25 production of important proteins or other products for commercial use, such as lipase, melanin, pigments, alkaloids, antibodies, hormones, pharmaceuticals, antibiotics and the like. Another useful phenotypic trait is the production of degradative or inhibitory enzymes, for example, enzymes preventing or inhibiting the root development in malting barley, or enzymes determining response or non-response to a systemically
30 administered drug in a human. The phenotypic trait may also be a secondary metabolite whose production is desired in a bioreactor.

Biochemical changes can also be determined by analytical methods, for example, in a high-throughput, fully automated fashion using robotics. Suitable biochemical analysis may include MALDI-TOF, LC/MS, GC/MS, two-dimensional IEF/SDS-PAGE, ELISA or other methods of analyses. The clones in the plant viral
5 vector library may then be functionally classified based on metabolic pathway affected or visual/selectable phenotype produced in the plant. This process enables a rapid determination of gene function for unknown nucleic acid sequences of a donor organism as well as a plant origin. Furthermore, this process can be used to rapidly confirm function of full-length DNA's of unknown function. Functional identification of
10 unknown nucleic acid sequences in a library of one organism may then rapidly lead to identification of similar unknown sequences in expression libraries for other organisms based on sequence homology. Such information is useful in many aspects including human medicine.

One useful means to determine the function of nucleic acids transfected into a
15 host is to observe the effects of gene silencing. Traditionally, functional gene knockout has been achieved following inactivation due to insertion of transposable elements or random integration of T-DNA into the chromosome, followed by characterization of conditional, homozygous-recessive mutants obtained upon backcrossing. Some teachings in these regards are provided by WO 97/42210 which is herein incorporated
20 by reference. As an alternative to traditional knockout analysis, an EST/DNA library from a donor organism, may be assembled into a plant viral transcription plasmid. The nucleic acid sequences in the transcription plasmid library may then be introduced into plant cells as part of a functional RNA virus which post-transcriptionally silences the homologous target gene. The EST/DNA sequences may be introduced into a plant viral
25 vector in either the plus or minus sense orientation, and the orientation can be either directed or random based on the cloning strategy. A high-throughput, automated cloning scheme based on robotics may be used to assemble and characterize the library. Alternatively, the EST/cDNA sequences can be inserted into the genomic RNA of a plant viral vector such that they are represented as genomic RNA during the viral
30 replication in plant cells. The library of EST clones is then transcribed into infectious RNAs and inoculated onto a host plant susceptible to viral infection. The viral RNAs containing the EST/cDNA sequences contributed from the original library are now

present in a sufficiently high concentration in the cytoplasm of host plant cells such that they cause post-transcriptional gene silencing of the endogenous gene in a host plant. Since the replication mechanism of the virus produces both sense and positive sense RNA sequences, the orientation of the EST/cDNA insert is normally irrelevant in terms of producing the desired phenotype in the host plant.

The present invention provides a method to express transiently viral-derived positive sense RNAs in transfected plants. Such method is much faster than the time required to obtain genetically engineered transgenic plants. Systemic infection and expression of viral positive sense RNA occurs as short as four days post inoculation, whereas it takes several months or longer to create a single transgenic plant. The invention provides a method to identify genes involved in the regulation of plant growth by inhibiting the expression of specific endogenous genes using viral vectors. This invention provides a method to characterize specific genes and biochemical pathways in donor organisms or in host plants using an RNA viral vector.

One problem with gene silencing in a plant host is that many plant genes exist in multigene families. Therefore, effective silencing of a gene function may be especially problematic. According to the present invention, however, nucleic acids may be inserted into the viral genome to effectively silence a particular gene function or to silence the function of a multigene family. It is presently believed that about 20% of plant genes exist in multigene families.

A detailed discussion of some aspects of the "gene silencing" effect is provided in the co-pending patent application, U.S. Patent Application Serial No. 08/260,546 (WO95/34668 published 12/21/95) the disclosure of which is incorporated herein by reference. RNA can reduce the expression of a target gene through inhibitory RNA interactions with target mRNA that occur in the cytoplasm and/or the nucleus of a cell.

It is known that silencing of endogenous genes can be achieved with homologous sequences from the same family. For example, Kumagai *et al.*, (*Proc. Natl. Acad. Sci. USA* 92:1679 (1995)) report that the *Nicotiana benthamiana* gene for phytoene desaturase (PDS) was silenced by transfection with a viral RNA derived from a clone containing a partial tomato (*Lycopersicon esculentum*) cDNA encoding PDS being in a positive sense orientation. This paper is incorporated here by reference. Kumagai *et al.* demonstrate that gene encoding PDS from one plant can be silenced by

transfecting a host plant with a nucleic acid of a known sequence, namely, a PDS gene, from a donor plant of the same family. The present invention provides a method of silencing a gene in a host plant by transfecting the host plant with a viral nucleic acid comprising a nucleic acid insert derived from a cDNA library or a genomic DNA or
5 RNA library from a non-plant organism. Different from Kumagai *et al*, the sequence of the nucleic acid insert in the present invention does not need to be identified or isolated prior to the transfection. Another feature of the present invention is that it provides a method to change the expression of a gene of a different family; the plus sense transcript of one plant results in enhancing or reducing expression of the endogenous gene or
10 multigene family of a plant of a different genus, family, order, class, subdivision, or division. The present invention is exemplified by overproduction of a GTP binding proteins. The present invention demonstrates that genes of one plant, such as *Arabidopsis*, which encode a GTP binding protein *Ran*, can be overexpressed in a different host plant by transfection the host plant with infectious RNAs containing
15 cDNA inserts from *Arabidopsis* cDNA library in a plus orientation, and result in host plant stunting. The present invention also demonstrates that a plant GTP binding protein is highly homologous to the GTP binding proteins from a non-plant organism such as a human, a frog, a mouse, a bovine, a fly and a yeast, not only at the amino acid level, but also at the nucleic acid level. The present invention thus provides a method to
20 change phenotype of a plant, by transfecting the plant with infectious RNAs derived from a homologous gene of a non-plant organism.

The invention is also directed to a method of determining a nucleic acid sequence in a donor organism from *Monera*, *Protista*, *Fungi* and *Animalia*, which has the same function as that in a host organism, by transfecting a nucleic acid sequence
25 derived from a donor organism into a host. In one preferred embodiment, the method comprising the steps of (a) preparing a library of cDNAs genomic DNAs or a pool of mRNAs of the donor organism, (b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from the library, (c) infecting each host with one of the recombinant viral nucleic acids, (d) growing the infected host, (e) detecting
30 one or more changes in the host, (f) identifying the recombinant viral nucleic acid that results in changes in the host, (g) determining the sequence of the nucleic acid insert in the recombinant viral nucleic acid that results in changes in the host, and (h)

determining the sequence of an entire open reading frame of the donor from which the nucleic acid insert is derived.

5 The invention is further directed to a method of determining a nucleic acid sequence in a host plant, which has the same function or homology as that in a donor organism from *Monera*, *Protista*, *Fungi* and *Animalia*, by transfecting a nucleic acid sequence derived from a donor organism into a host. In one preferred embodiment, the method comprising the steps of (a) preparing a cDNA library, a genomic DNA library, or a mRNA pool of the donor organism, (b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from the library, (c) infecting each host with
10 one of the recombinant viral nucleic acids, (d) growing the infected host, (e) detecting one or more changes in the host, (f) identifying the recombinant viral nucleic acid that results in changes in the host, (g) determining the sequence of the nucleic acid insert in the recombinant viral nucleic acid that results in changes in the host, and (h) determining the sequence of an entire open reading frame of a gene in the host, the expression of which gene is affected by the insert. The sequence of the nucleic acid insert in the cDNA clone or in the viral vector can be determined by a standard method, for example, by dideoxy termination using double stranded templates (Sanger *et al.*, *Proc., Natl. Acad. Sci. USA* 74:5463-5467 (1977)). Once the sequence of the nucleic acid insert is obtained, the sequence of an entire open reading frame of a gene can be
20 determined by probing filters containing full-length cDNAs from the cDNA library with the nucleic acid insert labeled with radioactive, fluorescent, or enzyme molecules. The sequence of an entire open reading frame of a gene can also be determined by RT-PCR (*Methods Mol. Biol.* 89:333-358 (1998)).

25 The present invention also provides a method of isolating a conserved gene from a donor organism such as *Monera*, *Protisca*, *Fungi* or *Animalia*. Libraries containing full-length cDNAs from fungi, and animals can be obtained from public and private sources or can be prepared from mRNAs. The cDNAs are inserted in viral vectors or in small subcloning vectors such as pBluescript (Stratagene), pUC18, M13, or pBR322. Transformed bacteria are then plated and individual clones selected by a standard method.
30 The bacteria transformants or DNAs are rearranged at high density onto membrane filters or glass slides. Full-length cDNAs can be identified by probing filters or slides with labeled

nucleic acid inserts which result in changes in a host plant. Useful labels include radioactive, fluorescent, or chemiluminescent molecules, enzymes, etc.

Alternatively, genomic libraries containing sequences from fungi, animals and libraries from retroviruses can be obtained from public and private sources, or be prepared
5 from plant genomic DNAs. BAC clones containing entire plant genomes have been constructed and organized in a minimal overlapping order. Individual BACs are sheared to fragments and directly cloned into viral vectors. Clones that completely cover an entire BAC form a BAC viral vector sublibrary. Genomic clones can be identified by probing filters containing BACs with labeled nucleic acid inserts which result in changes in a host
10 plant. Useful labels include radioactive, fluorescent, or chemiluminescent molecules, enzymes, etc. BACs that hybridize to the probe are selected and their corresponding BAC viral vectors are used to produce infectious RNAs. Plants that are transfected with the BAC sublibrary are screened for change of function, for example, change of growth rate or change of color. Once the change of function is observed, the inserts from these clones or
15 their corresponding plasmid DNAs are characterized by dideoxy sequencing. This provides a rapid method to obtain the genomic sequence of a donor organism. Using this method, once the DNA sequence in one organism is identified, it can be used to identify conserved sequences of similar function that exist in other libraries. This method speeds up the rate of discovering new genes.

20 The present invention provides a method to produce a non-plant protein in a plant. After DNAs of similar functions from a plant and a non-plant organism are isolated and identified, the amino acid sequences derived from the DNAs are compared. The plant DNA sequence is changed so that it encodes the same amino acid sequence as the DNA of the non-plant organism encodes. The DNA sequence can be changed
25 according to methods known to an ordinary skilled person, for example, site directed mutagenesis or DNA synthesis. One aspect of the invention is to provide a method of humanizing a plant cDNA. The method comprises selecting a plant cDNA that is homologous to human cDNA and making changes of the plant DNA, so that the modified plant cDNA expresses a human protein in a plant host. The production of
30 such human protein may be used in human medicine.

Nucleic acid sequences that may result in changing a plant phenotype include those involved in cell growth, proliferation, differentiation and development; cell

communication; and the apoptotic pathway. Genes regulating growth of cells or organisms include, for example, genes encoding a GTP binding protein, a ribosomal protein L19 protein, an S18 ribosomal protein, etc. Henry *et al.* (*Cancer Res.*, 53:1403-1408 (1993)) report that *erb B-2* (or *HER-2* or *neu*) gene was amplified and
5 overexpressed in one-third of cancers of the breast, stomach, and ovary; and the mRNA encoding the ribosomal protein L19 was more abundant in breast cancer samples that express high levels of *erbB-2*. Lijsebettens *et al.* (*EMBO J.*, 13:3378-3388 (1994)) report that in *Arabidopsis*, mutation at *PFL* caused pointed first leaves, reduced fresh weight and growth retardation. *PFL* codes for ribosomal protein S18, which has a high
10 homology with the rat S18 protein. Genes involved in development of cells or organisms include, for example, homeobox-containing genes and genes encoding G-protein-coupled receptor proteins such as the rhodopsin family. Homeobox genes are a family of regulatory genes containing a common 183-nucleotide sequence (homeobox) and coding for specific nuclear proteins (homeoproteins) that act as transcription
15 factors. The homeobox sequence itself encodes a 61-amino-acid domain, the homeodomain, responsible for recognition and binding of sequence-specific DNA motifs. The specificity of this binding allows homeoproteins to activate or repress the expression of batteries of down-stream target genes. Initially identified in genes controlling *Drosophila* development, the homeobox has subsequently been isolated in
20 evolutionarily distant animal species, plants, and fungi. Several indications suggest the involvement of homeobox genes in the control of cell growth and, when dysregulated, in oncogenesis (Cillo *et al.*, *Exp. Cell Res.*, 248:1-9 (1999)). Other nucleic acid sequences that may result in changes of a plant include genes encoding receptor proteins such as hormone receptors, cAMP receptors, serotonin receptors, and calcitonin family
25 of receptors; and light-regulated DNA encoding a leucine (Leu) zipper motif (Zheng *et al.*, *Plant Physiol.*, 116:27-35 (1998)). Deregulation or alteration of the process of cell growth, proliferation, differentiation and development; cell communication; and the apoptotic pathways may result in cancer. Therefore, identifying the nucleic acid sequences involved in those processes and determining their functions are beneficial to
30 the human medicine; it also provides a tool for cancer research.

This invention is exemplified by setting up a functional genomics screen using a Tobacco Mosaic Virus having a TMV-0 coat protein capsid for infection of *Nicotiana*

benthamiana, a plant related to the common tobacco plant. A human cDNA library is obtained from Clontech laboratories (Palo Alto, CA) on a "bacteria artificial chromosomes:" (BAC). The BACs are further subdivided into viral vector clones by inserting a section of cDNA at the 3' end of a subgenomic promoter of the viral vector.

5 The inserts are made in the antisense orientation as in Figure 1 until all of the cDNA from the BAC human cDNA library is represented on viral vectors. Each viral vector is sprayed onto the leaf of a 2 week old *N. benthamiana* plant with sufficient force to cause tissue injury and localized infection. Each infected plant is grown side by side with an uninfected plant and a plant infected with a null insert vector as control. All plants are
10 grown in an artificial environment having 16 hours of light and 8 hours of dark. Lumens are approximately equal on each plant. At intervals of 2 days, a visual and photographic observation of phenotype is made and recorded for each infected plant and each of its controls and a comparison is made. Data is entered into a Laboratory Information Management System database. At the end of the observation period severely stunted
15 plants, for example, are grouped for analysis. The nucleic acid insert contained in the viral vector clone 740AT #2441 is responsible for severe stunting of one of the plants. Clone 740AT #2481 is sequenced. The entire human cDNA sequence from which the insert was derived is obtained by sequencing and found to code for small GTP binding protein Ran 1. The #2441 DNA exhibits a high degree of homology (67% to 99%) to
20 tomato (*L. esculentum*), tobacco (*N. tabacum*), human, yeast, mouse and drosophila GTP binding proteins cDNAs The nucleotide sequence from 740 AT #2441 encodes a protein that has 67%-97% identities, and 79%-98% positives to other plants, yeast, mammalian such as human. This information is useful in pharmaceutical development as well as in toxicology studies.

25 Large amounts of DNA sequence information are being generated in the public domain, which may be entered into a relational database. Links may be made between sequences from various species predicted to carry out similar biochemical or regulatory functions. Links may also be generated between predicted enzymatic activities and visually displayed biochemical and regulatory pathways. Likewise, links may be
30 generated between predicted enzymatic or regulatory activity and known small molecule inhibitors, activators, substrates or substrate analogs. Phenotypic data from expression libraries expressed in transfected hosts may be automatically linked within

such a relational database. Genes with similar predicted roles of interest in other organisms may be rapidly discovered.

5 A complete classification scheme of gene functionality for a fully sequenced eukaryotic organism has been established for yeast. This classification scheme may be modified for other organisms and divided into the appropriate categories. Such organizational structure may be utilized to rapidly identify herbicide target loci which may confer dominant lethal phenotypes, and thereby is useful in helping to design rational herbicide programs.

10 The present invention is also directed to a method of increasing yield of a grain crop. In *Rice Biotechnology Quarterly* (37:4, (1999)), it is reported that a transgenic rice plant transformed with a *rgpl* gene, which encodes a small GTP binding protein from rice, was shorter than a control plant, but it produced more seeds than the control plant. To increase the yield of a grain crop, the present method comprises expressing a nucleic acid sequence of a non-plant organism in a positive sense orientation in the
15 cytoplasm of the grain crop, wherein said expressing results in stunted growth and increased seed production of said grain crop. A preferred method comprises the steps of cloning the nucleic acid sequence into a plant viral vector and infecting the grain crop with a recombinant viral nucleic acid comprising said nucleic acid sequence. Preferred plant viral vector is derived from a Brome Mosaic virus, a Rice Necrosis virus, or a
20 geminivirus. Preferred grain crops include rice, wheat, and barley. The nucleic acid expressed in the host plant, for example, comprises a GTP binding protein open reading frame having a positive sense orientation. The present method provides a transiently expression of a gene to obtain a stunted plant. Because less energy is put into plant growth, more energy is available for production of seed, which results in increase yield
25 of a grain crop. The present method has an advantage over other method using a transgenic plant, because it does not have an effect on the genome of a host plant.

In order to provide an even clearer and more consistent understanding of the specification and the claims, including the scope given herein to such terms, the following definitions are provided:

30 Adjacent: A position in a nucleotide sequence proximate to and 5' or 3' to a defined sequence. Generally, adjacent means within 2 or 3 nucleotides of the site of reference.

Anti-Sense Inhibition: A type of gene regulation based on cytoplasmic, nuclear or organelle inhibition of gene expression due to the presence in a cell of an RNA molecule complementary to at least a portion of the mRNA being translated. It is specifically contemplated that RNA molecules may be from either an RNA virus or mRNA from the host cells genome or from a DNA virus.

Cell Culture: A proliferating group of cells which may be in either an undifferentiated or differentiated state, growing contiguously or non-contiguously.

Chimeric Sequence or Gene: A nucleotide sequence derived from at least two heterologous parts. The sequence may comprise DNA or RNA.

Coding Sequence: A deoxyribonucleotide or ribonucleotide sequence which, when either transcribed and translated or simply translated, results in the formation of a cellular polypeptide or a ribonucleotide sequence which, when translated, results in the formation of a cellular polypeptide.

Compatible: The capability of operating with other components of a system. A vector or plant or animal viral nucleic acid which is compatible with a host is one which is capable of replicating in that host. A coat protein which is compatible with a viral nucleotide sequence is one capable of encapsidating that viral sequence.

Complementation Analysis: As used herein, this term refers to observing the changes produced in an organism when a nucleic acid sequence is introduced into that organism after a selected gene has been deleted or mutated so that it no longer functions fully in its normal role. A complementary gene to the deleted or mutated gene can restore the genetic phenotype of the selected gene.

Dual Heterologous Subgenomic Promoter Expression System (DHSPES): a plus stranded RNA vector having a dual heterologous subgenomic promoter expression system to increase, decrease, or change the expression of proteins, peptides or RNAs, preferably those described in U.S. Patent Nos. 5,316,931, 5,811,653, 5,589,367, and 5,866,785, the disclosure of which is incorporated herein by reference.

Expressed sequence tags (ESTs): Relatively short single-pass DNA sequences obtained from one or more ends of cDNA clones and RNA derived therefrom. They may be present in either the 5' or the 3' orientation. ESTs have been shown useful for identifying particular genes.

Expression: The term as used herein is meant to incorporate one or more of transcription, reverse transcription and translation.

A functional Gene Profile: The collection of genes of an organism which code for a biochemical or phenotypic trait. The functional gene profile of an organism is found by screening nucleic acid sequences from a donor organism by over expression or suppression of a gene in a host organism. A functional gene profile requires a collection or library of nucleic acid sequences from a donor organism. A functional gene profile will depend on the ability of the collection or library of donor nucleic acids to cause over-expression or suppression in the host organism. Therefore, a functional gene profile will depend upon the quantity of donor genes capable of causing over-expression or suppression of host genes or of being expressed in the host organism in the absence of a homologous host gene.

Gene: A discrete nucleic acid sequence responsible for producing one or more cellular products and/or performing one or more intercellular or intracellular functions.

Gene silencing: A reduction in gene expression. A viral vector expressing gene sequences from a host may induce gene silencing of homologous gene sequences.

Homology: A degree of nucleic acid similarity in all or some portions of a gene sequence sufficient to result in gene suppression when the nucleic acid sequence is delivered in the positive sense orientation.

Host: A cell, tissue or organism capable of replicating a nucleic acid such as a vector or plant viral nucleic acid and which is capable of being infected by a virus containing the viral vector or viral nucleic acid. This term is intended to include prokaryotic and eukaryotic cells, organs, tissues or organisms, where appropriate. Bacteria, fungi, yeast, animal (cell, tissues, or organisms), and plant (cell, tissues, or organisms) are examples of a host.

Infection: The ability of a virus to transfer its nucleic acid to a host or introduce a viral nucleic acid into a host, wherein the viral nucleic acid is replicated, viral proteins are synthesized, and new viral particles assembled. In this context, the terms "transmissible" and "infective" are used interchangeably herein. The term is also meant to include the ability of a selected nucleic acid sequence to integrate into a genome, chromosome or gene of a target organism.

5 Multigene family: A set of genes descended by duplication and variation from some ancestral gene. Such genes may be clustered together on the same chromosome or dispersed on different chromosomes. Examples of multigene families include those which encode the histones, hemoglobins, immunoglobulins, histocompatibility antigens, actins, tubulins, keratins, collagens, heat shock proteins, salivary glue proteins, chorion proteins, cuticle proteins, yolk proteins, and phaseolins.

10 Non-Native: Any RNA or DNA sequence that does not normally occur in the cell or organism in which it is placed. Examples include recombinant plant viral nucleic acids and genes or ESTs contained therein. That is, an RNA or DNA sequence may be non-native with respect to a viral nucleic acid. Such an RNA or DNA sequence would not naturally occur in the viral nucleic acid. Also, an RNA or DNA sequence may be non-native with respect to a host organism. That is, such a RNA or DNA sequence would not naturally occur in the host organism.

15 Nucleic acid: As used herein the term is meant to include any DNA or RNA sequence from the size of one or more nucleotides up to and including a complete gene sequence. The term is intended to encompass all nucleic acids whether naturally occurring in a particular cell or organism or non-naturally occurring in a particular cell or organism.

20 Nucleic acid of interest: The term is intended to refer to the nucleic acid sequence whose function is to be determined. The sequence will normally be non-native to a viral vector but may be native or non-native to a host organism.

Phenotypic Trait: An observable, measurable or detectable property resulting from the expression or suppression of a gene or genes.

25 Plant Cell: The structural and physiological unit of plants, consisting of a protoplast and the cell wall.

Plant Organ: A distinct and visibly differentiated part of a plant, such as root, stem, leaf or embryo.

30 Plant Tissue: Any tissue of a plant in planta or in culture. This term is intended to include a whole plant, plant cell, plant organ, protoplast, cell culture, or any group of plant cells organized into a structural and functional unit.

Positive-sense inhibition: A type of gene regulation based on cytoplasmic inhibition of gene expression due to the presence in a cell of an RNA molecule substantially homologous to at least a portion of the mRNA being translated.

Promoter: The 5'-flanking, non-coding sequence substantially adjacent a coding
5 sequence which is involved in the initiation of transcription of the coding sequence.

Protoplast: An isolated plant or bacterial cell without some or all of its cell wall.

Recombinant Plant Viral Nucleic Acid: Plant viral nucleic acid which has been modified to contain non-native nucleic acid sequences. These non-native nucleic acid
10 sequences may be from any organism or purely synthetic, however, they may also include nucleic acid sequences naturally occurring in the organism into which the recombinant plant viral nucleic acid is to be introduced.

Recombinant Plant Virus: A plant virus containing the recombinant plant viral nucleic acid.

Subgenomic Promoter: A promoter of a subgenomic mRNA of a viral nucleic
15 acid.

Substantial Sequence Homology: Denotes nucleotide sequences that are substantially functionally equivalent to one another. Nucleotide differences between such sequences having substantial sequence homology are insignificant in affecting function of the gene products or an RNA coded for by such sequence.

Systemic Infection: Denotes infection throughout a substantial part of an
20 organism including mechanisms of spread other than mere direct cell inoculation but rather including transport from one infected cell to additional cells either nearby or distant.

Transposon: A nucleotide sequence such as a DNA or RNA sequence which is
25 capable of transferring location or moving within a gene, a chromosome or a genome.

Transgenic Plant: A plant which contains a foreign nucleotide sequence inserted into either its nuclear genome or organellar genome.

Transient Expression: Expression of a nucleic acid sequence in a host without insertion of the nucleic acid sequence into the host genome, such as by way of a viral
30 vector.

Transcription: Production of an RNA molecule by RNA polymerase as a complementary copy of a DNA sequence or subgenomic mRNA.

Vector: A self-replicating RNA or DNA molecule which transfers an RNA or DNA segment between cells, such as bacteria, yeast, plant, or animal cells.

Virus: An infectious agent composed of a nucleic acid which may or may not be encapsidated in a protein. A virus may be a mono-, di-, tri-, or multi-partite virus, as
5 described above.

EXAMPLES

The following examples further illustrate the present invention. These examples are intended merely to be illustrative of the present invention and are not to be construed as being limiting.

10 EXAMPLE 1

Gene silencing/co-suppression of genes induced by delivering an RNA capable of base pairing with itself to form double stranded regions.

Gene silencing has been used to down regulate gene expression in transgenic plants. Recent experimental evidence suggests that double stranded RNA may be an
15 effective stimulator of gene silencing/co-suppression phenomenon in transgenic plant. For example, Waterhouse *et al.* (*Proc. Natl. Acad. Sci. USA* 95:13959-13964 (1998), incorporated herein by reference) described that virus resistance and gene silencing in plants could be induced by simultaneous expression of sense and antisense RNA. Gene silencing/co-suppression of plant genes may be induced by delivering an RNA capable
20 of base pairing with itself to form double stranded regions.

This example shows: (1) a novel method for generating an RNA virus vector capable of producing an RNA capable of forming double stranded regions, and (2) a process to silence plant genes by using such a viral vector.

Step 1: Construction of a DNA sequence which after it is transcribed would
25 generate an RNA molecule capable of base pairing with itself. Two identical, or nearly identical, ds DNA sequences are ligated together in an inverted orientation to each other (i.e., in either a head to tail or tail to head orientation) with or without a linking nucleotide sequence between the homologous sequences. The resulting DNA sequence is then be cloned into a cDNA copy of a plant viral vector genome.

30 Step 2: Cloning, screening, transcription of clones of interest using known methods in the art.

Step 3: Infect plant cells with transcripts from clones.

As virus expresses foreign gene sequence, RNA from foreign gene forms base pair upon itself, forming double-stranded RNA regions. This approach is used with any plant or non-plant gene and used to silence plant gene homologous to assist in
5 identification of the function of a particular gene sequence.

EXAMPLE 2

Expression of cDNAs encoding tomato phytoene synthase and phytoene desaturase in *Nicotiana benthamiana*.

Isolation of tomato mosaic virus cDNA. An 861 base pair fragment (5524-6384) from
10 the tomato mosaic virus (fruit necrosis strain F; tom-F) containing the putative coat protein subgenomic promoter, coat protein gene, and the 3'-end was isolated by PCR using primers 5'-CTCGCAAAGTTTCGAACCAAATCCTC-3' (upstream) (SEQ ID NO: 1) and 5'-CGGGGTACCTGGGCCCCAACCGGGGGTTCGCGGGG-3' (downstream) (SEQ ID NO: 2) and subcloned into the *HincII* site of pBluescript KS-. A
15 hybrid virus consisting of TMV-U1 and ToMV-F was constructed by swapping an 874-bp *BamHI-KpnI* ToMV fragment into pBGC152, creating plasmid TTO1. The inserted fragment was verified by dideoxynucleotide sequencing. A unique *AvrII* site was inserted downstream of the *XhoI* site in TTO1 by PCR mutagenesis, creating plasmid TTO1A, using the following oligonucleotides: 5'-
20 TCCTCGAGCCTAGGCTCGCAAAGTTTCGAACCAAATCCTCA-3' (upstream) (SEQ ID NO: 3), 5'-CGGGGTACCTGGGCCCCAACCGGGGGTTCGCGGGG-3' (downstream) (SEQ ID NO: 4).

Isolation of a cDNA encoding tomato phytoene synthase and a partial cDNA encoding tomato phytoene desaturase. Partial cDNAs were isolated from ripening tomato fruit
25 RNA by polymerase chain reaction (PCR) using the following oligonucleotides: *PSY*, 5'-TATGTATGGTGCAGAAGAACAGAT-3' (upstream) (SEQ ID NO: 5), 5'-AGTCGACTCTTCCTCTTCTGGCAT C-3' (downstream) (SEQ ID NO: 6); *PDS*, 5'-TGCTCGAGTGTGTTCTTCAGTTTCTGTCA-3' (SEQ ID NO: 7) (upstream), 5'-AACTCGAGCGCTTTGATTCTCCGAAGCTT-3' (downstream) (SEQ ID NO: 8).
30 Approximately 3 X 10⁴ colonies from a *Lycopersicon esculentum* cDNA library were

screened by colony hybridization using a ³²P labeled tomato phytoene synthase PCR product. Hybridization was carried out at 42°C for 48 hours in 50% formamide, 5X SSC, 0.02 M phosphate buffer, 5X Denhart's solution, and 0.1 mg/ml sheared calf thymus DNA. Filters were washed at 65°C in 0.1X SSC, 0.1% SDS prior to
5 autoradiography. PCR products and the phytoene synthase cDNA clones were verified by dideoxynucleotide sequencing.

DNA sequencing and computer analysis. A *Pst*I, BamHI fragment containing the phytoene synthase cDNA and the partial phytoene desaturase cDNA was subcloned into pBluescript® KS+ (Stratagene, La Jolla, California). The nucleotide sequencing of
10 KS+/PDS #38 and KS+/ 5'3'PSY was carried out by dideoxy termination using single-stranded templates (Maniatis, *Molecular Cloning*, 1st Ed.) Nucleotide sequence analysis and amino acid sequence comparisons were performed using PCGENE® and DNA Inspector® IIE programs.

Construction of the tomato phytoene synthase expression vector. A *Xho*I fragment
15 containing the tomato phytoene synthase cDNA was subcloned into TTO1. The vector TTO1/PSY + (FIGURE 1, SEQ ID NOs: 9 and 10) contains the phytoene synthase cDNA in the positive orientation under the control of the TMV-U1 coat protein subgenomic promoter; while, the vector TTO1/PSY - contains the phytoene synthase cDNA in the antisense orientation.

Construction of a viral vector containing a partial tomato phytoene desaturase cDNA. A
20 *Xho*I fragment containing the partial tomato phytoene desaturase cDNA was subcloned into TTO1. The vector TTO1A/PDS + (FIGURE 2) contains the phytoene desaturase cDNA in the positive orientation under the control of the TMV-U1 coat protein subgenomic promoter; while the vector TTO1A/PDS - contains the phytoene desaturase
25 cDNA in the antisense orientation.

Analysis of *N. benthamiana* transfected by TTO1/PSY+, TTO1/PSY-, TTO1A/PDS +, TTO1A/PDS -. Infectious RNAs from TTO1/PSY+, TTO1/PSY-, TTO1A/PDS +, and TTO1A/PDS - were prepared by *in vitro* transcription using SP6 DNA-dependent RNA polymerase as described previously (Dawson *et al.*, *Proc. Natl. Acad. Sci. USA* **85**:1832

(1986)) and were used to mechanically inoculate *N. benthamiana*. The hybrid viruses spread throughout all the non-inoculated upper leaves as verified by transmission electron microscopy, local lesion infectivity assay, and polymerase chain reaction (PCR) amplification. The viral symptoms resulting from the infection consisted of distortion of systemic leaves and plant stunting with mild chlorosis. The leaves from plants transfected with TTO1/PSY+ turned orange and accumulated high levels of phytoene while those transfected with TTO1/PDS+ and TTO1/PDS- turned white. Agarose gel electrophoresis of PCR cDNA isolated from virion RNA and Northern blot analysis of virion RNA indicate that the vectors are maintained in an extrachromosomal state and have not undergone any detectable intramolecular rearrangements.

Purification and analysis of carotenoids from transfected plants. The carotenoids were isolated from systemically infected tissue and analyzed by HPLC chromatography. Carotenoids were extracted in ethanol and identified by their peak retention time and absorption spectra on a 25-cm Spherisorb® ODS-15- m column using acetonitrile/methanol/2-propanol (85:10:5) as a developing solvent at a flow rate of 1 ml/min. They had identical retention time to a synthetic phytoene standard and β -carotene standards from carrot and tomato. The phytoene peak from *N. benthamiana* transfected with TTO1/PSY + had an optical absorbance maxima at 276, 285, and 298 nm. Plants transfected with viral encoded phytoene synthase showed a ten-fold increase in phytoene compared to the levels in noninfected plants. The expression of sense and antisense RNA to a partial phytoene desaturase in transfected plants increased the level of phytoene and altered the biochemical pathway; it thus inhibited the synthesis of colored carotenoids and caused the systemically infected leaves to turn white. HPLC analysis of these plants revealed that they also accumulated phytoene. The white leaf phenotype was also observed in plants treated with the herbicide norflurazon which specifically inhibits phytoene desaturase.

This change in the levels of phytoene represents one of the largest increases of any carotenoid (secondary metabolite) in any genetically engineered plant. Plants transfected with viral-encoded phytoene synthase in a plus sense showed a ten-fold increase in phytoene compared to the levels in noninfected plants. In addition, the accumulation of phytoene in plants transfected with antisense phytoene desaturase

suggests that viral vectors can be used as a potent tool to manipulate pathways in the production of secondary metabolites through cytoplasmic antisense inhibition. Leaves from systemically infected TT01A/PDS+ plants also accumulated phytoene and developed a bleaching white phenotype; the actual mechanism of inhibition is not clear.

5 These data are presented by Kumagai *et al.*, *Proc. Natl. Acad. Sci. USA* 92:1679-1683 (1995).

EXAMPLE 3

Expression of bell pepper cDNA in transfected plant confirms that it encodes capsanthin-capsorubin synthase.

10 The biosynthesis of leaf carotenoids in *Nicotiana benthamiana* was altered by rerouting the pathway to the synthesis of capsanthin, a non-native chromoplast-specific xanthophyll, using an RNA viral vector. A cDNA encoding capsanthin-capsorubin synthase (Ccs), was placed under the transcriptional control of a tobamovirus subgenomic promoter. Leaves from transfected plants expressing Ccs developed an

15 orange phenotype and accumulated high levels of capsanthin. This phenomenon was associated by thylakoid membrane distortion and reduction of grana stacking. In contrast to the situation prevailing in chromoplasts, capsanthin was not esterified and its increased level was balanced by a concomitant decrease of the major leaf xanthophylls, suggesting an autoregulatory control of chloroplast carotenoid composition. Capsanthin

20 was exclusively recruited into the trimeric and monomeric light-harvesting complexes of Photosystem II. This demonstration that higher plant antenna complexes can accommodate non-native carotenoids provides compelling evidence for functional remodeling of photosynthetic membranes by rational design of carotenoids.

Construction of the Ccs expression vector. Unique *Xho*I, *Avr*II sites were inserted into

25 the bell pepper capsanthin-capsorubin synthase (Ccs) cDNA by polymerase chain reaction (PCR) mutagenesis using oligonucleotides: 5'-GCCTCGAGTGCAGCATGGAAACCCTTCTAAAGCTTTTCC-3' (upstream) (SEQ ID NO: 11), 5'-TCCCTAGGTCAAAGGCTCTCTATTGCTAGATTGCCC-3' (downstream) (SEQ ID NO: 12). The 1.6-kb *Xho*I, *Avr*II cDNA fragment was placed

30 under the control of the TMV-U1 coat protein subgenomic promoter by subcloning into

TT01A, creating plasmid TT01A CCS+ (FIGURE 3) in the sense orientation as represented by FIGURE 3.

Carotenoid analysis. Twelve days after inoculation upper leaves from 12 plants were harvested and lyophilized. The resulting non-saponified extract was evaporated to dryness under argon and weighed to determine the total lipid content. Pigment analysis from the total lipid content was performed by HPLC and also separated by thin layer chromatography on silica gel G using hexane / acetone (60:40 (V/V)). Plants transfected with TT01A CCS+ accumulated high levels of capsanthin (36% of total carotenoids).

10

EXAMPLE 4

Expression of bacterial *CrtB* gene in transfected plants confirms that it encodes phytoene synthase.

We developed a new viral vector, TTU51, consisting of tobacco mosaic virus strain U1 (TMV-U1) (Goelet *et al.*, *Proc. Natl. Acad. Sci. USA* 79:5818-5822 (1982)), and tobacco mild green mosaic virus (TMGMV; U5 strain) (Solis *et al.*, "The complete nucleotide sequence of the genomic RNA of the tobamovirus tobacco mild green mosaic virus" (1990)). The open reading frame (ORF) for *Erwinia herbicola* phytoene synthase (*CrtB*) (Armstrong *et al.*, *Proc. Natl. Acad. Sci. USA* 87:9975-9979 (1990)) was placed under the control of the tobacco mosaic virus (TMV) coat protein subgenomic promoter in the vector TTU51. This construct also contained the gene encoding the chloroplast targeting peptide (CTP) for the small subunit of ribulose-1,5-bisphosphate carboxylase (RUBISCO) (O'Neal *et al.*, *Nucl. Acids Res.* 15:8661-8677 (1987)) and was called TTU51 CTP *CrtB* as represented by FIGURE 4. Infectious RNA was prepared by *in vitro* transcription using SP6 DNA-dependent RNA polymerase (Dawson *et al.*, *Proc. Natl. Acad. Sci. USA* 83:1832-1836 (1986)); Susek *et al.*, *Cell* 74:787-799 (1993)) and was used to mechanically inoculate *N. benthamiana*. The hybrid virus spread throughout all the non-inoculated upper leaves and was verified by local lesion infectivity assay and polymerase chain reaction (PCR) amplification. The leaves from plants transfected with TTU51 CTP *CrtB* developed an orange pigmentation that spread systemically during plant growth and viral replication.

Leaves from plants transfected with TTU51 CTP *CrtB* had a decrease in chlorophyll content (result not shown) that exceeded the slight reduction that is usually observed during viral infection. Since previous studies have indicated that the pathways of carotenoid and chlorophyll biosynthesis are interconnected (Susek *et al.*, *Cell* 74:787-799 (1993)), we decided to compare the rate of synthesis of phytoene to chlorophyll. Two weeks post-inoculation, chloroplasts from plants infected with TTU51 CTP *CrtB* transcripts were isolated and assayed for enzyme activity. The ratio of phytoene synthetase to chlorophyll syntheses was 0.55 in transfected plants and 0.033 in uninoculated plants (control). Phytoene synthase activity from plants transfected with TTU51 CTP *CrtB* was assayed using isolated chloroplasts and labeled [¹⁴C] geranylgeranyl PP. There was a large increase in phytoene and an unidentified C₄₀ alcohol in the *CrtB* plants.

Phytoene synthetase assay.

The chloroplasts were prepared as described previously (Camara, *Methods Enzymol.* 214:352-365 (1993)). The phytoene synthase assays were carried out in an incubation mixture (0.5 ml final volume) buffered with Tris-HCL, pH 7.6, containing [¹⁴C] geranylgeranyl PP (100,000 cpm) (prepared using pepper GGPP synthase expressed in *E. coli*), 1 mM ATP, 5 mM MnCl₂, 1 mM MgCl₂, Triton X-100 (20 mg per mg of chloroplast protein) and chloroplast suspension equivalent to 2 mg protein. After 2 h incubation at 30°C, the reaction products were extracted with chloroform methanol (Camara, *supra*) and subjected to TLC onto silicagel plate developed with benzene/ethyl acetate (90/10) followed by autoradiography.

Chlorophyll synthetase assay.

For the chlorophyll synthetase assay, the isolated chloroplasts were lysed by osmotic shock before incubation. The reaction mixture (0.2 ml, final volume) consisting of 50 mM Tris-HCL (pH 7.6) containing [¹⁴C] geranylgeranyl PP (100,000 cpm), 5 MgCl₂, 1 mM ATP, and ruptured plasmid suspension equivalent to 1 mg protein was incubated for 1 hr at 30°C. The reaction products were analyzed as described previously.

Plasmid Constructions.

The chloroplast targeting, phytoene synthase expression vector, TTU51 CTP *CrtB* as represented in FIGURE 5, was constructed in several subcloning steps. First, a unique *Sph*I site was inserted in the start codon for the *Erwinia herbicola* phytoene synthase gene by polymerase chain reaction (PCR) mutagenesis (Saiki *et al.*, *Science* 230:1350-1354 (1985)) using oligonucleotides *CrtB* M1S 5'-CCA AGC TTC TCG AGT GCA GCA TGC AGC AAC CGC CGC TGC TTG AC-3' (upstream) (SEQ ID NO: 13) and *CrtB* P300 5'-AAG ATC TCT CGA GCT AAA CGG GAC GCT GCC AAA GAC CGG CCG G-3' (downstream) (SEQ ID NO: 14). The *CrtB* PCR fragment was subcloned into pBluescript® (Stratagene) at the *Eco*RV site, creating plasmid pBS664. A 938 bp *Sph*I, *Xho*I *CrtB* fragment from pBS664 was then subcloned into a vector containing the sequence encoding the *N. tabacum* chloroplast targeting peptide (CTP) for the small subunit of RUBISCO, creating plasmid pBS670. Next, the tobamoviral vector, TTU51, was constructed. A 1020 base pair fragment from the tobacco mild green mosaic virus (TMGMV; U5 strain) containing the viral subgenomic promoter, coat protein gene, and the 3'-end was isolated by PCR using TMGMV primers 5'-GGC TGT GAA ACT CGA AAA GGT TCC GG-3' (upstream) (SEQ ID NO: 15) and 5'-CGG GGT ACC TGG GCC GCT ACC GGC GGT TAG GGG AGG-3' (downstream) (SEQ ID NO: 16), subcloned into the *Hinc*II site of Bluescript KS-, and verified by dideoxynucleotide sequencing. This clone contains a naturally occurring duplication of 147 base pairs (SEQ ID NO: 17) that includes the whole upstream pseudoknot domain in the 3' noncoding region. The hybrid viral cDNA consisting of TMV-U1 and TMGMV was constructed by swapping a 1-Kb *Xho*I-*Kpn*I TMGMV fragment into TTO1 (Kumagai *et al.*, *Proc. Natl. Acad. Sci. USA* 92:1679-1683 (1995)), creating plasmid TTU51. Finally, the 1.1 Kb *Xho*I CTP *CrtB* fragment from pBS670 was subcloned into the *Xho*I of TTU51, creating plasmid TTU51 CTP *CrtB*. As a CTP negative control, a 942 bp *Xho*I fragment containing the *CrtB* gene from pBS664 was subcloned into TTU51, creating plasmid TTU51 *CrtB* #15.

EXAMPLE 5

Construction of a tobamoviral vector for expression of heterologous genes in *A. thaliana*.

Virions that were prepared as a crude aqueous extract of tissue from turnip
5 infected with Ribgrass mosaic virus (RMV) were used to inoculate *N. benthamiana*, *N. tabacum*, *A. thaliana*, and oilseed rape (canola). Two to three weeks after transfection, systemically infected plants were analyzed by immunoblotting, using purified RMV as a standard. Total soluble plant protein concentrations were determined using bovine serum albumin as a standard. The proteins were analyzed on a 0.1% SDS/12.5%
10 polyacrylamide gel and transferred by electroblotting for 1 hr to a nitrocellulose membrane. The blotted membrane was incubated for 1 hr with a 2000-fold dilution of anti-ribgrass mosaic virus coat antiserum. Using standard protocols, the antisera was raised in rabbits against purified RMV coat protein. The enhanced chemiluminescence horseradish peroxidase-linked, goat anti-rabbit IgG assay (Cappel Laboratories) was
15 performed according to the manufacturer's (Amersham) specifications. The blotted membrane was subjected to film exposure times of up to 10 sec. No detectable cross-reacting protein was observed in the noninfected *N. benthamiana* control plant extracts. A 18 kDa protein cross-reacted to the anti-RMV coat antibody from systemically infected *N. benthamiana*, *N. tabacum*, *A. thaliana*, and oilseed rape (canola). This result
20 demonstrates that RMV can systemically infect *N. benthamiana*, *N. tabacum*, *A. thaliana*, and oilseed rape (canola).

Plasmid constructions.

Ribgrass mosaic virus (RMV) is a member of the tobamovirus group that infects crucifers. A partial RMV cDNA containing the 30K subgenomic promoter, 30K ORF,
25 coat subgenomic promoter, coat ORF, and 3'-end was isolated by RT-PCR using oligonucleotides TVCV183X, 5'-TAC TCG AGG TTC ATA AGA CCG CGG TAG GCG G-3' (upstream) (SEQ ID NO: 18) and TVCV KpnI, 5'-CGG GGT ACC TGG GCC CCT ACC CGG GGT TTA GGG AGG-3' (downstream) (SEQ ID NO: 19), and subcloned into the EcoRV site of KS+, creating plasmid KS+ TVCV #23 (FIGURE 5).
30 The RMV cDNA was characterized by restriction mapping and dideoxy nucleotide sequencing. The partial nucleotide sequence is as follows:

5'-

CTCGAGGTTTCATAAGACCGCGGTAGGCGGAGCGTTTGTCTTACTGTAGTATAA
TTAAATATTTGTCAGATAAAAGGTTGTTTAAAGATTTGTTTTTTGTTTGACTG
AGTCGATAATGTCTTACGAGCCTAAAGTTAGTGACTTCCTTGCTCTTACGAA
5 AAAGGAGGAAATTTTACCCAAGGCTTTGACGAGATTAAAGACTGTCTCTATT
AGTACTAAGGATGTTATATCTGTTAAGGAGTCTGAGTCCCTGTGTGATATTG
ATTTGTTAGTGAATGTGCCATTAGATAAGTATAGGTATGTGGGTGTTTTGGG
TGTTGTTTTTACCGGTGAATGGCTGGTACCGGATTTTCGTTAAAGGTGGGGTA
ACAGTGAGCGTGATTGACAAACGGCTTGAAAATTCCAGAGAGTGCATAATT
10 GGTACGTACCGAGCTGCTGTAAAGGACAGAAGGTTCCAGTTCAAGCTGGTT
CCAAATTACTTCGTATCCATTGCGGATGCCAAGCGAAAACCGTGGCAGGTT
CATGTGCGAATTCAAATCTGAAGATCGAAGCTGGATGGCAACCTCTAGCT
CTAGAGGTGGTTTTCTGTTGCCATGGTTACTAATAACGTGGTTGTTAAAGGTT
TGAGGGAAAAGGTCATCGCAGTGAATGATCCGAACGTGCAAGGTTTCGAAG
15 GTGTGGTTGACGATTTTCGTCGATTCGGTTGCTGCATTCAAGGCGATTGACAG
TTTCCGAAAGAAAAAGAAAAAGATTGGAGGAAGGGATGTAAATAATAATA
AGTATAGATATAGACCGGAGAGATACGCCGGTCCTGATTCGTTACAATATA
AAGAAGAAAATGGTTTACAACATCACGAGCTCGAATCAGTACCAGTATTTTC
GCAGCGATGTGGGCAGAGCCCACAGCGATGCTTAACCAGTGCCTGTCTGCG
20 TTGTCGCAATCGTATCAAACCTCAGGCGGCAAGAGATACTGTTAGACAGCAG
TTCTCTAACCTTCTGAGTGCGATTGTGACACCGAACCAGCGGTTTCCAGAAA
CAGGATACCGGGTGTATATTAATTCAGCAGTTCTAAAACCGTTGTACGAGTC
TCTCATGAAGTCCTTTGATACTAGAAATAGGATCATTGAAACTGAAGAAGA
GTCGCGTCCATCGGCTTCCGAAGTATCTAATGCAACACAACGTGTTGATGAT
25 GCGACCGTGGCCATCAGGAGTCAAATTCAGCTTTTGCTGAACGAGCTCTCCA
ACGGACATGGTCTGATGAACAGGGCAGAGTTCGAGGTTTTATTACCTTGGG
CTACTGCGCCAGCTACATAGGCGTGGTGCACACGATAGTGCATAGTGTTTTT
CTCTCCACTTAAATCGAAGAGATATACTTACGGTGTAATTCGCAAGGGTG
CGTAAACCAAATTACGCAATGTTTTAGGTTCCATTTAAATCGAAACCTGTTA
30 TTTCTGGATCACCTGTTAACGTACGCGTGGCGTATATTACAGTGGGAATAA
CTAAAAGTGAGAGGTTTCAATCCTCCCTAACCCCGGGTAGGGGCCCA-
3'(SEQ ID NO: 20).

The 1543 base pair from the partial RMV cDNA was compared (PCGENE) to oilseed rape mosaic virus (ORMV). The nucleotide sequence identity was 97.8%. The RMV 30K and coat ORF were compared to ORMV and the amino acid identity was 98.11% (30K) and 98.73% (coat), respectively. A partial RMV cDNA containing the 5'-end and part of the replicase was isolated by RT-PCR from RMV RNA using oligonucleotides RGMV1 5'-GAT GGC GCC TTA ATA CGA CTC ACT ATA GTT TTA TTT TTG TTG CAA CAA CAA CAA C-3' (upstream) (SEQ ID NO: 21) and RGR 132 5'-CTT GTG CCC TTC ATG ACG AGC TAT ATC ACG-3' (downstream) (SEQ ID NO: 22). The RMV cDNA was characterized by dideoxy nucleotide sequencing. The partial nucleotide sequence containing the T7 RNA polymerase promoter and part of the RMV cDNA is as follows:

5'-
ccttaatacgaactcactataGTTTTATTTTTGTTGCAACAACAACAACAATTACAATAA
CAACAAAACAAATACAAACAACAACAACATGGCACAATTTCAACAAACAG
15 TAAACATGCAAACATTGCAGGCTGCCGCAGGGCGCAACAGCCTGGTGAATG
ATTTAGCCTCACGACGTGTTTATGACAATGCTGTCTGAGGAGCTAAATGCACG
CTCGAGACGCCCTAAGGTTTATTACTCCAAATCAGTGTCTACGGAACAGAC
GCTGTTAGCTTCAAACGCTTATCCGGAGTTTGAGATTTCTTTACTCATACCC
AACATGCCGTACACTCCCTTGCGGGTGGCCTAAGGACTCTTGAGTTAGAGTA
20 TCTCATGATGCAAGTTCCGTTCTCGTTCTCTGACGTACGACATCGGTGGTAAC
TTTGCAGCGCACCTTTTCAAAGGACGCGACTACGTTCACTGCTGTATGCCAA
ACTTGGATGTACGTGATATAGCT-3' (SEQ ID NO: 23). The uppercase letters are nucleotide sequences from RMV cDNA. The lower case letters are nucleotide sequences from T7 RNA polymerase promoter. The nucleotide sequences from the 5' and 3' oligonucleotides are underlined.

Full-length infectious RMV cDNA clones were obtained by RT-PCR from RMV RNA using oligonucleotides RGMV1, 5'-GAT GGC GCC TTA ATA CGA CTC ACT ATA GTT TTA TTT TTG TTG CAA CAA CAA CAA C-3' (upstream) (SEQ ID NO: 24) and RG1 APE, 5'-ATC GTT TAA ACT GGG CCC CTA CCC GGG GTT AGG GAG G-3' (downstream) (SEQ ID NO: 25). The RMV cDNA was characterized by dideoxy nucleotide sequencing. The partial nucleotide sequence containing the T7 RNA polymerase promoter and part of the RMV cDNA is as follows:

5'-

CCTTAATACGACTCACTATAGTTTTATTTTGTGCAACAACAACAACAAAT
TACAATAACAACAAAACAAATACAAACAACAACATGGCACAATTTCAA
CAAACAGTAAACATGCAAACATTCCAGGCTGCCGCAGGGCGCAACAGCCTG
5 GTGAATGATTTAGCCTCACGACGTGTTTATGACAATGCTGTGAGGAGCTAA
ATGCACGCTCGAGACGCCCTAAGGTTCACTCCAAATCAGTGTCTACGGA
ACAGACGCTGTTAGCTTCAAACGCTTATCCGGAGTTTGAGATTTCTTTACT
CATACCCAAACATGCCGTACACTCCCTTGCGGGTGGCCTAAGGACTCTTGAG
TTAGAGTATCTCATGATGCAAGTTCCGTTTCGGTCTCTGACGTACGACATCG
10 GTGGTAACTTTGCAGCGCACCTTTTCAAAGGACGCGACTACGTTCACTGCTG
TATGCCAAACTTGATGTACGTGATATAGCT-3' (SEQ ID NO: 26). The
uppercase letters are nucleotide sequences from RMV cDNA. The nucleotide sequences
from the 5' and 3' oligonucleotides are underlined. Full length infectious RMV cDNA
clones were obtained by RT-PCR from RMV RNA using oligonucleotides RGMV1, 5'-
15 gat ggc gcc tta ata cga ctc act ata gtt tta ttt ttg ttg caa caa caa caa c-3' (upstream) (SEQ
ID NO: 27) and RG1 APE, 5'-ATC GTT TAA ACT GGG CCC CTA CCC GGG GTT
AGG GAG G-3' (downstream) (SEQ ID NO: 28).

EXAMPLE 6

Expression of methylotrophic yeast *ZZA1* gene in transfected plants confirms that it
20 encodes alcohol oxidase.

A genomic clone encoding alcohol oxidase *ZZA1*, the first enzyme involved in
methanol utilization, was isolated from a newly described *Pichia pastoris* strain.
Kumagai *et al.*, *Bio/Technology* 11:606-610 (1993). Sequence analysis indicates that
gene encodes a polypeptide of approximately 72-kDa. Comparison of the amino acid
25 sequence to *Pichia pastoris AOX1* and *AOX2* alcohol oxidases indicates that they show
97.4% and 96.4% similarity to each other, respectively. The open reading frame (ORF)
for alcohol oxidase, from the a genomic clone containing *ZZA1*, was placed under the
control of the tobamoviral subgenomic promoter in TTO1A, a hybrid tobacco mosaic
virus (TMV) and tomato mosaic virus (ToMV) vector. Infectious RNA from TTO1SAI
30 APE *ZZA1* (FIGURE 6) was prepared by *in vitro* transcription using SP6 DNA-
dependent RNA polymerase and used to mechanically inoculate *N. benthamiana*. The

72-kDa protein accumulated in systemically infected tissue and was analyzed by immunoblotting, using *Pichia pastoris* alcohol oxidase as a standard. No detectable cross-reacting protein was observed in the noninfected *N. benthamiana* control plant extracts.

5 Isolation of the alcohol oxidase gene.

Three hundred nanograms of the yeast *Pichia pastoris* genomic DNA digested with *Pst*I and *Xho*I was amplified by PCR using a 25-mer oligonucleotide (5'-TTG CAC TCT GTT GGC TCA TGA CGA T-3') (SEQ ID NO: 29) corresponding to the nucleotide sequence of *AOX1* promoter and a 26-mer oligonucleotide (5'-CAA GCT
10 TGC ACA AAC GAA CGT CTC AC-3') (SEQ ID NO: 30) corresponding to a nucleotide sequence derived from the *AOX1* terminator. The PCR conditions using *Thermus aquaticus* DNA polymerase (2.5U; Perkin-Elmer Cetus) consisted of an initial 2 minute incubation at 97°C followed by two cycles at 97°C (1min.), 45°C (1min.), 60°C (1 min.), thirty-five cycles at 94°C (1 min.), 45°C (1 min.), 60°C (1 min.), and a
15 final DNA polymerase extension at 60°C for 7 min. The 3273 base pair fragment containing *ZZA1* gene was phenol/chloroform treated and precipitated with ammonium acetate/ethanol. After digestion with *Sac*I the fragment was purified by 1% low melt agarose electrophoresis and subcloned into the *Sac*I/*Eco*RV sites in pBluescript KS-. The alcohol oxidase genomic clone KS-AO7'8' was characterized by restriction
20 mapping and dideoxynucleotide sequencing.

Plasmid Constructions.

Unique *Xho*I, *Avr*II sites were inserted into the *Pichia pastoris* clone KS-AO7'8' by polymerase chain reaction (PCR) mutagenesis using oligonucleotides: 5'-CAC TCG AGA GCA TGG CTA TTC CCG AAG AAT TTG ATA TTA TCG-3' (upstream) (SEQ
25 ID NO: 31) and 5'-TCC CTA GGT TAG AAT CTA GCA AGA CCG GTC TTC TCG-3' (downstream) (SEQ ID NO: 32). The 2.0-kb *Xho*I, *Avr*II *ZZA1* PCR fragment was subcloned into pTTO1APE, creating plasmid TTO1APE *ZZA1*.

EXAMPLE 7

Arabidopsis thaliana cDNA library construction in a dual subgenomic promoter vector.

30 *Arabidopsis thaliana* cDNA libraries obtained from the *Arabidopsis* Biological

Resource Center (ABRC). The four libraries from ABRC were size-fractionated with inserts of 0.5-1 kb (CD4-13), 1-2 kb (CD4-14), 2-3 kb (CD4-15), and 3-6 kb (CD4-16). All libraries are of high quality and have been used by several dozen groups to isolate genes. The pBluescript® phagemids from the Lambda ZAP II vector were subjected to
5 mass excision and the libraries were recovered as plasmids according to standard procedures.

Alternatively, the cDNA inserts in the CD4-13 (Lambda ZAP II vector) were recovered by digestion with *NotI*. Digestion with *NotI* in most cases liberated the entire *Arabidopsis thaliana* cDNA insert because the original library was assembled with *NotI*
10 adapters. *NotI* is an 8-base cutter that infrequently cleaves plant DNA. In order to insert the *NotI* fragments into a transcription plasmid, the pBS735 transcription plasmid (FIGURE 7) was digested with *PacI/XhoI* and ligated to an adapter DNA sequence created from the oligonucleotides 5'-TCGAGCGGCCGCAT-3' (SEQ ID NO: 33) and 5'-GCGGCCGC-3' (SEQ ID NO: 159). The resulting plasmid pBS740 (FIGURE 8)
15 contains a unique *NotI* restriction site for bidirectional insertion of *NotI* fragments from the CD4-13 library. Recovered colonies were prepared from these for plasmid minipreps with a Qiagen BioRobot 9600®. The plasmid DNA preps performed on the BioRobot 9600® are done in 96-well format and yield transcription quality DNA. An *Arabidopsis* cDNA library was transformed into the plasmid and analyzed by agarose
20 gel electrophoresis to identify clones with inserts. Clones with inserts are transcribed *in vitro* and inoculated onto *N. benthamiana* or *Arabidopsis thaliana*. Selected leaf disks from transfected plants are then taken for biochemical analysis.

EXAMPLE 8

25 High throughput robotics.

The efficiency of inoculation of subject organisms such as plants is improved by using means of high throughput robotics. For example, host plants such as *Arabidopsis thaliana* were grown in microtiter plates such as the standard 96-well and 384-well microtiter plates. A robotic handling arm then moved the plates containing the
30 organism to a colony picker or other robot that delivered inoculations to each plant in the well. By this procedure, inoculation was performed in a very high speed and high

throughput manner. It is preferable that the plant is a germinating seed or at least in the development cycle to enable access to the cells to be transfected. Equipments used for automated robotic production line include, but not be limited to, robots of these types: electronic multichannel pipetmen, Qiagen BioRobot 9600®, Robbins Hydra liquid handler, Flexys Colony Picker, New Brunswick automated plate pourer, GeneMachines HiGro shaker incubator, New Brunswick floor shaker, three Qiagen BioRobots, MJ Research PCR machines (PTC-200, Tetrad), ABI 377 sequencer and Tecan Genesis RSP200 liquid handler.

EXAMPLE 9

- 10 Expression of chinese cucumber cDNA clone pQ21D in transfected plants confirms that it encodes α -trichosanthin.

We have developed a plant viral vector that directs the expression of α -trichosanthin in transfected plants. The open reading frame (ORF) for α -trichosanthin, from the genomic clone SEO, was placed under the control of the TMV coat protein subgenomic promoter. Infectious RNA from TTU51A QSEO #3 (FIGURE 9) was prepared by *in vitro* transcription using SP6 DNA-dependent RNA polymerase and was used to mechanically inoculate *N. benthamiana*. The hybrid virus spread throughout all the non-inoculated upper leaves as verified by local lesion infectivity assay, and PCR amplification. The viral symptoms consisted of plant stunting with mild chlorosis and distortion of systemic leaves. The 27-kDa α -trichosanthin accumulated in upper leaves (14 days after inoculation) and cross-reacted with an anti-trichosanthin antibody.

Plasmid Constructions.

An 0.88-kb *Xho*I, *Avr*II fragment, containing the α -trichosanthin coding sequence, was amplified from genomic DNA isolated from *Trichosanthes kirilowii* Maximowicz by PCR mutagenesis using oligonucleotides QMIX: 5'-GCC TCG AGT GCA GCA TGA TCA GAT TCT TAG TCC TCT CTT TGC-3' (upstream) (SEQ ID NO: 34) and Q1266A 5'-TCC CTA GGC TAA ATA GCA TAA CTT CCA CAT CA AAGC-3' (downstream) (SEQ ID NO: 35). The α -trichosanthin open reading frame was verified by dideoxy sequencing, and placed under the control of the TMV-U1 coat

protein subgenomic promoter by subcloning into TTU51A, creating plasmid TTU51A QSEO #3.

In vitro Transcriptions, Inoculations, and Analysis of Transfected Plants.

N. benthamiana plants were inoculated with *in vitro* transcripts of *Kpn* I-
5 digested TTU51A QSEO #3 as previously described (Dawson *et al.*, *supra*). Virions
were isolated from *N. benthamiana* leaves infected with TTU51A QSEO #3 transcripts.

Purification, Immunological Detection, and in vitro Assay of α -Trichosanthin.

Two weeks after inoculation, total soluble protein was isolated from upper,
noninoculated *N. benthamiana* leaf tissue and assayed from cross-reactivity to a α -
10 trichosanthin antibody. The proteins from systemically infected tissue were analyzed on
a 0.1% SDS/12.5% polyacrylamide gel and transferred by electroblotting for 1 hr to a
nitrocellulose membrane. The blotted membrane was incubated for 1 hr with a 2000-
fold dilution of goat anti- α -trichosanthin antiserum. The enhanced chemiluminescence
horseradish peroxidase-linked, rabbit anti-goat IgG assay (Cappel Laboratories) was
15 performed according to the manufacturer's (Amersham) specifications. The blotted
membrane was subjected to film exposure times of up to 10 sec. Shorter and longer
chemiluminescent exposure times of the blotted membrane gave the same quantitative
results.

EXAMPLE 10

20 Expression and targeting to the chloroplasts of a green fluorescent protein in
Arabidopsis thaliana via a recombinant viral nucleic acid vector.

The gene encoding green fluorescent protein (GFP) was fused at the N-terminus
to the chloroplast transit peptide (CTP) sequence of RuBPCase to create plasmid
pBS723 (FIGURE 10). Plasmid pBS723 was modified by PCR mutagenesis to create a
25 unique *Pac*I site upstream of the ATG start codon of the CTP-GFP gene fusion. The
PCR amplification product obtained from plasmid pBS723 was digested *Pac*I/*Sal*II and
cloned into plasmid GFP-30B/clone 60 (also digested with *Pac*I/*Sal*II) to create plasmid
pBS731 (FIGURE 11). Plasmid pBS731 was linearized at a unique *Kpn*I restriction site
and transcribed into infectious RNA with T7 RNA polymerase according to standard
30 procedures. Infectious RNA transcripts that were inoculated onto *Nicotiana*

benthamiana plants showed systemic expression in the upper leaves of CTP-GFP within six days. Plants infected with RNA transcripts from plasmid pBS731 were harvested by grinding the leaves with a mortar and pestle to obtain recombinant virions derived from pBS731 infectious RNA transcripts. Virions from pBS731 were inoculated onto

5 *Arabidopsis thaliana* leaves. The inoculated leaves of *Arabidopsis thaliana* plants showed strong green fluorescence under UV light, thus indicating successful expression of the CTP-GFP reporter gene.

EXAMPLE 11

Production of a malarial CTL epitope genetically fused to the C terminus of the

10 TMVCP.

Malarial immunity induced in mice by irradiated sporozites of *P. yoelii* is also dependent on CD8+ T lymphocytes. Clone B is one cytotoxic T lymphocyte (CTL) cell clone shown to recognize an epitope present in both the *P. yoelii* and *P. berghei* CS proteins. Clone B recognizes the following amino acid sequence;

15 SYVPSAEQILEFVKQISSQ (SEQ ID NO: 36) and when adoptively transferred to mice, it protects against infection from both species of malaria sporozoites. Construction of a genetically modified tobamovirus designed to carry this malarial CTL epitope fused to the surface of virus particles is set forth herein.

Construction of plasmid pBGC289. A 0.5 kb fragment of pBGC11 was PCR amplified

20 using the 5' primer TB2ClaI5' and the 3' primer C/-5AvrII. The amplified product was cloned into the *Sma*I site of pBstKS+ (Stratagene Cloning Systems) to form pBGC214.

PBGC215 was formed by cloning the 0.15 kb *Acc*I-*Nsi*I fragment of pBGC214 into pBGC235. The 0.9 kb *Nco*I-*Kpn*I fragment from pBGC215 was cloned in

25 pBGC152 to form pBGC216.

A 0.07 kb synthetic fragment was formed by annealing PYCS.2p with PYCS.2m and the resulting double stranded fragment, encoding the *P. yoelii* CTL malarial epitope, was cloned into the *Avr*II site of pBGC215 made blunt ended by treatment with mung bean nuclease and creating a unique *Aat*II site, to form pBGC262. A 0.03 kb

30 synthetic *Aat*II fragment was formed by annealing TLS.1EXP with TLS.1EXM, and the

resulting double stranded fragment, encoding the leaky-stop sequence and a stuffer
sequence used to facilitate cloning, was cloned into *Aat*II digested pBGC262 to form
pBGC263. PBGC262 was digested with *Aat*II and ligated to itself removing the 0.02 kb
stuffer fragment to form pBGC264. The 1.0 kb *Nco*I-*Kpn*I fragment of pBGC264 was
5 cloned into pSNC004 to form pBGC289.

The virus TMV289 produced by transcription of plasmid pBGC289 *in vitro*
contains a leaky stop signal resulting in the removal of four amino acids from the C
terminus of the wild type TMV coat protein gene and is therefore predicted to
synthesize a truncated coat protein and coat protein with a CTL epitope fused at the C
10 terminus at a ratio of 20:1. The recombinant TMVCP/CTL epitope fusion present in
TMV289 is with the stop codon decoded as the amino acid Y (amino acid residue 156).
The amino acid sequence of the coat protein of virus TMV216 produced by
transcription of the plasmid pBGC216 *in vitro*, is truncated by four amino acids. The
epitope SYVPSAEQILEFVKQISSQ is calculated to be present at approximately 0.5%
15 of the weight of the virion using the same assumptions confirmed by quantitative
ELISA analysis.

Propagation and purification of the epitope expression vector. Infectious
transcripts were synthesized from *Kpn*I-linearized pBGC289 using T7 RNA polymerase
and cap (7mGpppG) according to the manufacturer (New England Biolabs).

20 An increased quantity of recombinant virus was obtained by passaging Sample
ID No. TMV289.11B1a. Fifteen tobacco plants were grown for 33 days post
inoculation accumulating 595 g fresh weight of harvested leaf biomass not including the
two lower inoculated leaves. Purified Sample ID No. TMV289.11B2 was recovered
(383 mg) at a yield of 0.6 mg virion per gram of fresh weight. Therefore, 3 g of 19-mer
25 peptide was obtained per gram of fresh weight extracted. Tobacco plants infected with
TMV289 accumulated greater than 1.4 micromoles of peptide per kilogram of leaf
tissue.

Product analysis. Partial confirmation of the sequence of the epitope coding region of
TMV289 was obtained by restriction digestion analysis of PCR amplified cDNA using
30 viral RNA isolated from Sample ID No. TMV289.11B2. The presence of proteins in
TMV289 with the predicted mobility of the cp fusion at 20 kD and the truncated cp at
17.1 kD was confirmed by denaturing polyacrylamide gel electrophoresis.

EXAMPLE 12

Genomic DNA library construction in a recombinant viral nucleic acid vector.

Genomic DNAs represented in BAC (bacterial artificial chromosome) or YAC (yeast artificial chromosome) libraries are obtained from the *Arabidopsis* Biological
5 Resource Center (ABRC). The BAC/YAC DNAs are mechanically size-fractionated, ligated to adapters with cohesive ends, and shotgun-cloned into recombinant viral nucleic acid vectors. Alternatively, mechanically size-fractionated genomic DNAs are blunt-end ligated into a recombinant viral nucleic acid vector. Recovered colonies are prepared for plasmid minipreps with a Qiagen BioRobot 9600®. The plasmid DNA
10 preps done on the BioRobot 9600® are assembled in 96-well format and yield transcription quality DNA. The recombinant viral nucleic acid/*Arabidopsis* genomic DNA library is analyzed by agarose gel electrophoresis (template quality control step) to identify clones with inserts. Clones with inserts are then transcribed *in vitro* and inoculated onto *N. benthamiana* and/or *Arabidopsis thaliana*. Selected leaf disks from
15 transfected plants are then be taken for biochemical analysis.

Genomic DNA from *Arabidopsis* typically contains a gene every 2.5 kb (kilobases) on average. Genomic DNA fragments of 0.5 to 2.5 kb obtained by random shearing of DNA were shotgun assembled in a recombinant viral nucleic acid expression/knockout vector library. Given a genome size of *Arabidopsis* of
20 approximately 120,000 kb, a random recombinant viral nucleic acid genomic DNA library would need to contain minimally 48,000 independent inserts of 2.5 kb in size to achieve 1X coverage of the *Arabidopsis* genome. Alternatively, a random recombinant viral nucleic acid genomic DNA library would need to contain minimally 240,000 independent inserts of 0.5 kb in size to achieve 1X coverage of the *Arabidopsis*
25 genome. Assembling recombinant viral nucleic acid expression/knockout vector libraries from genomic DNA rather than cDNA has the potential to overcome known difficulties encountered when attempting to clone rare, low-abundance mRNA's in a cDNA library. A recombinant viral nucleic acid expression/knockout vector library made with genomic DNA would be especially useful as a gene silencing knockout
30 library. In addition, the Dual Heterologous Subgenomic Promoter Expression System (DHSPES) expression/knockout vector library made with genomic DNA would be especially useful for expression of genes lacking introns. Furthermore, other plant

species with moderate to small genomes (e.g. rose, approximately 80,000 kb) would be especially useful for recombinant viral nucleic acid expression/knockout vector libraries made with genomic DNA. A recombinant viral nucleic acid expression/knockout vector library can be made from existing BAC/YAC genomic DNA or from
5 newly-prepared genomic DNAs for any plant species.

EXAMPLE 13

Genomic DNA or cDNA library construction in a DHSPES vector, and transfection of individual clones from said vector library onto T-DNA tagged or transposon tagged or mutated plants.

10 Genomic DNA or cDNA library construction in a recombinant viral nucleic acid vector, and transfection of individual clones from the vector library onto T-DNA tagged or transposon tagged or mutated plants may be performed according the procedure set forth in Example 6. Such a protocol may be easily designed to complement mutations introduced by random insertional mutagenesis of T-DNA sequences or transposon
15 sequences.

EXAMPLE 14

Identification of nucleotide sequences involved in the regulation of plant growth by cytoplasmic inhibition of gene expression using viral derived RNA.

In the following examples, we show: (1) a method for producing plus sense
20 RNA using an RNA viral vector, (2) a method to produce viral-derived sense RNA in the cytoplasm, (3) a method to enhance or suppress the expression of endogenous plant proteins in the cytoplasm by viral antisense RNA, and (4) a method to produce transfected plants containing viral plus sense RNA; such methods are much faster than the time required to obtain genetically engineered sense transgenic plants. Systemic
25 infection and expression of viral plus sense RNA occurs as short as four days post inoculation, whereas it takes several months or longer to create a single transgenic plant. These examples demonstrates that novel positive strand viral vectors, which replicate solely in the cytoplasm, can be used to identify genes involved in the regulation of plant growth by enhancing or inhibiting the expression of specific endogenous genes. These

examples enable one to characterize specific genes and biochemical pathways in transfected plants using an RNA viral vector.

5 Tobamoviral vectors have been developed for the heterologous expression of uncharacterized nucleotide sequences in transfected plants. A partial *Arabidopsis*
10 *thaliana* cDNA library was placed under the transcriptional control of a tobamovirus subgenomic promoter in a RNA viral vector. Colonies from transformed *E. coli* were automatically picked using a Flexys robot and transferred to a 96 well flat bottom block containing terrific broth (TB) Amp 50 ug/ml. Approximately 2000 plasmid DNAs were isolated from overnight cultures using a BioRobot and infectious RNAs from 430
15 independent clones were directly applied to plants. One to two weeks after inoculation, transfected *Nicotiana benthamiana* plants were visually monitored for changes in growth rates, morphology, and color. One set of plants transfected with 740 AT #2441 were severely stunted. DNA sequence analysis revealed that this clone contained an *Arabidopsis* Ran GTP binding protein open reading frame (ORF) in a plus sense
20 orientation. This demonstrates that an episomal RNA viral vector can be used to deliberately alter the metabolic pathway and cause plant stunting. In addition, our results show that the *Arabidopsis* plus sense transcript can cause phenotypic changes in *N. benthamiana*.

Construction of an *Arabidopsis thaliana* cDNA library in an RNA viral vector.

20 An *Arabidopsis thaliana* CD4-13 cDNA library was digested with *NotI*. DNA fragments between 500 and 1000 bp were isolated by trough elution and subcloned into the *NotI* site of pBS740. *E. coli* C600 competent cells were transformed with the pBS740 AT library and colonies containing *Arabidopsis* cDNA sequences were selected on LB Amp 50 ug/ml. Recombinant C600 cells were automatically picked using a
25 Flexys robot and then transferred to a 96 well flat bottom block containing terrific broth (TB) Amp 50 ug/ml. Approximately 2000 plasmid DNAs were isolated from overnight cultures using a BioRobot (Qiagen) and infectious RNAs from 430 independent clones were directly applied to plants.

Isolation of a gene encoding a GTP binding protein.

30 One to two weeks after inoculation, transfected *Nicotiana benthamiana* plants were visually monitored for changes in growth rates, morphology, and color. Plants

transfected with 740 AT #2441 (FIGURE 12) were severely stunted. Plasmid 740 AT #2441 contains the TMV-U1 open reading frames (ORFs) encoding 126-, 183-, and 30-kDa proteins, the TMV-U5 coat protein gene (U5 cp), the T7 promoter, an *Arabidopsis thaliana* CD4-13 NotI fragment, and part of the pUC19 plasmid. The TMV-U1 subgenomic promoter located within the minus strand of the 30-kDa ORF controls the synthesis of the CD4-13 subgenomic RNA.

DNA sequencing and computer analysis.

A 841 bp NotI fragment of 740 AT #2441 (FIGURE 13, SEQ ID NOs: 37 and 38) containing the Ran GTP binding protein cDNA was characterized. The nucleotide sequencing of 740 AT #2441 was carried out by dideoxy termination using double stranded templates (Sanger *et al.* 1977). Nucleotide sequence analysis and amino acid sequence comparisons were performed using DNA Strider, PCGENE and NCBI Blast programs. 740 AT #2441 contained an open reading frame (ORF) in the positive orientation that encodes a protein of 221 amino acids with an apparent molecular weight of 25,058 Da. The mass of the protein was calculated using the X program (Perceptive Biosystems). FIGURE 14 shows the nucleotide sequence alignment of 740AT #2441 to AF017991, a *A. thaliana* salt stress inducible small GTP binding protein Ran1 (SEQ ID NO: 39). FIGURE 15 shows the nucleotide alignment of 740 AT #2441 to L16787, a *N. tabacum* small ras-like GTP binding protein (SEQ ID NO: 40). FIGURE 16 shows the amino acid comparison of 740 AT #2441 (SEQ ID NO: 41) to tobacco Ran-B1 GTP binding protein (SEQ ID NO: 42). The #2441 DNA exhibits a high degree of homology (67% to 83%) to tomato (*L. esculentum*), tobacco (*N. tabacum*), human, yeast, mouse and drosophila GTP binding proteins cDNAs (Table 1). The nucleotide sequence from 740 AT #2441 encodes a protein that has 67%-97% identities, and 79%-98% positives to other plants, yeast, mammalian such as human (Table 2).

MALDI-TOF analysis of *N. benthamiana* transfected with 740 AT #2441

10 days after inoculation, the apical meristem, leaves, and stems from *N. benthamiana* transfected with 740 AT #2441, were frozen in liquid nitrogen. The soluble proteins were extracted in grinding buffer (100mM Tris, pH 7.5, 2 mM EDTA, 1 mM PMSF, 10 mM BME) using a mortar and pestle. The homogenate was filtered through four layers of cheesecloth and spun at 10, 000 X g for 15 min. The supernatant

was decanted and spun at 100,000 X g for 1 hr. A 500 µl aliquot of the supernant was mixed with 500 µl 20% TCA (acetone/0.07% BME) and stored at 4° C overnight. The supernant was analyzed by MALDI-TOF (Karas *et al.*, *Anal. Chem.*, 60:230 (1988)). The results showed that the soluble proteins contained a newly expressed protein of
5 molecular weight 25,058.

Isolation of an *Arabidopsis thaliana* GTP binding protein genomic clone

A genomic clone encoding *A. thaliana* GTP binding proteins can be isolated by probing filters containing *A. thaliana* BAC clones using a ³²P-labelled 740 AT #2441 *NotI* insert. Other members of the *A. thaliana* ARF multigene family have been
10 identified using programs of the University of Wisconsin Genetic Computer Group.

Table 1. 740 AT #2441 Nucleotide sequence comparison

<u>Clone</u>	<u>Score</u>	<u>Pvalue</u>	<u>Identities</u>	<u>Positives</u>
<i>A thaliana</i> AF017991	3645 (1007.2 bits)	0.00E+00	733/738 (99%)	733/738 (99%)
<i>L. escutentum</i> L28714	2341 (646.9 bits)	1.50E-189	561/677 (82%)	561/677 (82%)
<i>N. tabacum</i> L16787	2336 (645.5 bits)	3.90E-189	556/667 (83%)	556/667 (83%)
Human ras-like protein mRNA M31469	1383 (383.1 bits)	1.10E-107	427/615 (69%)	427/615 (69%)
Yeast GTP-binding protein L-08690	1394 (385.2 bits)	3.90E-106	430/619 (69%)	430/619 (69%)
Mouse GTPase (Ran) mRNA L32751	1338 (369.7 bits)	1.30E-101	422/615 (68%)	422/615 (68%)
<i>C. elegans</i> RAN/TC4 mRNA U66216	1002 (276.9 bits)	2.70E-75	274/366 (74%)	274/366 (74%)
<i>D. discoideum</i> TC4/RAN mRNA L09720	979 (270.5 bits)	3.10E-71	323/482 (67%)	323/482 (67%)

Table 2. 740 AT #2441 Amino acid sequence comparison

<u>Clone</u>	<u>Score</u>	<u>Pvalue</u>	<u>Identities</u>	<u>Positives</u>
<i>A. thaliana</i> SP_PL:O04664	1192 (554.1 bits)	1.50E-162	221/221 (100%)	221/221 (100%)
<i>N. tabacum</i> SW:RANA_TOBAC P41918	1169 (543.4 bits)	2.50E-159	216/221 (97%)	218/221 (98%)
<i>L. esculentum</i> SW:RAN2_LYCES P38547	1148 (533.7 bits)	2.20E-156	212/221 (95%)	214/221 (96%)
<i>S. cerevisiae</i> P32836	899 (417.9 bits)	1.10E-125	165/217 (76%)	186/217 (85%)
<i>C. elegans</i> O17915	891 (414.2 bits)	2.10E-120	167/207 (80%)	181/207 (87%)
<i>M. musculus</i> P28746	885 (397.4 bits)	2.20E-115	159/205 (77%)	175/205 (85%)
<i>H. sapiens</i> GTP-binding protein P17080	849 (394.7 bits)	1.50E-114	158/205 (77%)	174/205 (84%)
<i>Plasmodium falciparum</i> P38545	716 (332.8 bits)	3.10E-102	129/176 (73%)	151/176 (85%)
<i>D. discoideum</i> GTP-binding protein P33519	760 (353.3 bits)	4.50E-102	138/204 (67%)	163/204 (79%)

EXAMPLE 15

Construction of a cytoplasmic inhibition vector containing *A. thaliana* ribulose biphosphate carboxylase small subunit (Rubisco) nucleotide sequence.

An *Arabidopsis thaliana* CD4-13 cDNA library was digested with *NotI*. DNA
5 fragments between 500 and 1000 bp were isolated by trough elution and subcloned into the
NotI site of pBS740. *E. coli* C600 competent cells were transformed with the pBS740 AT
library and colonies containing *Arabidopsis* cDNA sequences were selected on LB Amp 50
µg/ml.

Isolation of a gene encoding ribulose biphosphate carboxylase (Rubisco) small subunit.

10 One to two weeks after inoculation, transfected *Nicotiana benthamiana* plants
were visually monitored for changes in growth rates, morphology, and color. Plants
transfected with 740 AT #1191 (FIGURE 17) developed etched yellow concentric rings
around the systemically infected veins. Plasmid 740 AT #1191 contains the TMV-U1
126-, 193-, and 30-kDa ORFs, the TMV-U5 coat protein gene (U5 cp), the T7
15 promoter, an *Arabidopsis thaliana* CD4-13 *NotI* fragment, and part of the pUC19
plasmid. The TMV-U1 subgenomic promoter located within the minus strand of the
30-kDa ORF controls the syntehsis of the CD4-13 subgenomic RNA.

DNA sequencing and computer analysis.

The *NotI* fragment of 740 AT #1191 was characterized: nucleotide sequence
20 analysis and amino acid sequence comparisons were performed using DNA Strider,
PCGENE and NCBI Blast programs. 740 AT #1191 contained a partial open reading frame
(ORF) of Rubisco in the positive orientation (FIGURE 18, SEQ ID NO. 43), the start codon
of which is deleted from the wild type. 740 AT #1191 encodes a partial *A. thaliana*
ribulose biphosphate carboxylase (FIGURE 18, SEQ ID NO: 44) which is a highly
25 expressed protein in plants. The expression of Rubisco was inhibited in the transfected *N.*
benthamiana because 740 AT #1191 contained only a partial Ribisco small unit cDNA,
without a start codon.

EXAMPLE 16

Construction of a cytoplasmic inhibition vector containing *A. thaliana* HAT7 homeobox-leucine zipper nucleotide sequence.

An *Arabidopsis thaliana* CD4-13 cDNA library was digested with *NotI*. DNA
5 fragments between 500 and 1000 bp were isolated by trough elution and subcloned into the *NotI* site of pBS740. *E. coli* C600 competent cells were transformed with the pBS740 AT library and colonies containing *Arabidopsis* cDNA sequences were selected on LB Amp 50 µg/ml.

Isolation of a gene encoding HAT7 homeobox-leucine zipper.

10 One to two weeks after inoculation, transfected *Nicotiana benthamiana* plants were visually monitored for changes in growth rates, morphology, and color. Plants transfected with 740 AT #855 (FIGURE 19) were moderately stunted. Plasmid 740 AT #855 contains the TMV-U1 126-, 193-, and 30-kDa ORFs, the TMV-U5 coat protein gene (U5 cp), the T7 promoter, an *Arabidopsis thaliana* CD4-13 *NotI* fragment, and part
15 of the pUC19 plasmid. The TMV-U1 subgenomic promoter located within the minus strand of the 30-kDa ORF controls the syntehsis of the CD4-13 subgenomic RNA.

DNA sequencing and computer analysis.

The *NotI* fragment of 740 AT #855 was characterized: nucleotide sequence
analysis and amino acid sequence comparisons were performed using DNA Strider,
20 PCGENE and NCBI Blast programs 740 AT #855 contained *A. thaliana* HAT 7 homeobox-luecine zipper cDNA sequence. The nucleotide sequence alignment of 740 AT #855 and *Arabidopsis thaliana* HAT7 homeobox protein ORF (UO9340) was compared. FIGURE 20 shows the nucleotide sequences of 740 #855 (SEQ ID NO: 45) and *A. thaliana* HAT7 homeobox protein ORF (SEQ ID NO: 46), and the amino acid
25 sequence of *A. thaliana* HAT7 homeobox protein ORFs (SEQ ID NO: 47). The result show that 740 AT #855 contains a 3'- untranslated region (UTR) of the *A. thaliana* HAT7 homeobox protein ORF in a positive orientation, thus inhibited the expression of HAT 7 homeobox protein in the transfected *N. benthamiana*. Table 3 shows the 740 AT #855 nucleotide sequence comparison with *A. thaliana*, rat and human: 65-98%
30 identities and positives are shown.

Table 3. 740 AT #855 Nucleotide sequence comparison

<u>Clone</u>	<u>Score</u>	<u>Pvalue</u>	<u>Identities</u>	<u>Positives</u>
<i>A thaliana</i> clone HAT7 U09340	847 (234.01 bits)	1.80E+60	171/173 (98%)	171/173 (98%)
Rat mRNA ribosomal protein L32 X06483	728 (201.2 bits)	5.70E-51	248/376 (65%)	248/376 (65%)
Human mRNA for ribosomal protein L32 X0334	728 (201.2 bits)	8.00E-51	248/376 (65%)	248/376 (65%)

EXAMPLE 17

Construction of a *Nicotiana benthamiana* cDNA library.

Vegetative *N. benthamiana* plants were harvested 3.3 weeks after sowing and sliced up into three groups of tissue: leaves, stems and roots. Each group of tissue was flash frozen in liquid nitrogen and total RNA was isolated from each group separately using the following hot borate method (Larry Smart and Thea Wilkins, 1995). Frozen tissue was ground to a fine powder with a pre-chilled mortar and pestle, and then further homogenized in pre-chilled glass tissue grinder. Immediately thereafter, 2.5 ml/g tissue hot (~82°C) XT Buffer (0.2 M borate decahydrate, 30 mM EGTA, 1% (w/v) SDS. Adjusted pH to 9.0 with 5 N NaOH, treated with 0.1% DEPC and autoclaved. Before use, added 1% deoxycholate (sodium salt), 10 mM dithiothreitol, 15 Nonidet P-40 (NP-40) and 2% (w/v) polyvinylpyrrolidone, MW 40,000 (PVP-40)) was added to the ground tissue. The tissue was homogenized 1-2 minutes and quickly decanted to a pre-chilled Oak Ridge centrifuge tube containing 105 µl of 20 mg/ml proteinase K in DEPC treated water. The tissue grinder was rinsed with an additional 1 ml hot XT Buffer per g tissue, which was then added to rest of the homogenate. The homogenate was incubated at 42°C at 100 rpm for 1.5 h. 2 M KCl was added to the homogenate to a final concentration of 160 mM, and the mixture was incubated on ice for 1 h to precipitate out proteins. The homogenate was centrifuged at 12,000 x g for 20 min at 4°C, and the supernatant was filtered through sterile miracloth into a clean 50 ml Oak Ridge centrifuge tube. 8 M LiCl was added to a final concentration of 2 M LiCl and incubated on ice overnight. Precipitated RNA was collected by centrifugation at 12,000 x g for 20 min at 4°C. The pellet was washed three times in 3-5 ml 4°C 2 M LiCl. Each time the pellet was resuspended with a glass rod and then spun at 12,000 x g for 20 min at 4°C. The RNA pellet was suspended in 2 ml 10 mM Tris-HCl (pH 7.5), and purified from insoluble cellular components by spinning at 12,000 x g for 20 min at 4°C. The RNA containing supernatant was transferred to a 15 ml Corex tube and precipitated overnight at -20°C with 2.5 volumes of 100 % ethanol. The RNA was pelleted by centrifugation at 9,800 x g for 30 min at 4°C. The RNA pellet was washed in 1-2 ml cold 70°C ethanol and centrifuged at 9,800 x g for 5 min at 4°C. Residual ethanol was removed from the RNA pellet under vacuum, and the RNA was resuspended in 200 µl DEPC treated dd-water and transferred to a 1.5 ml microfuge tube. The Corex tube was rinsed

in 100 µl DEPC-treated dd-water, which was then added to the rest of the RNA. The RNA was then precipitated with 1/10 volume of 3 M sodium acetate, pH 6.0 and 2.5 volumes of cold 100% ethanol at -20°C for 1-2 h. The tube was centrifuged for 20 min at 16,000 x g, and the RNA pellet washed with cold 70% ethanol, and centrifuged for 5 min at 16,000 x g. After drying the pellet under vacuum, the RNA was resuspended in DEPC-treated water. This is the total RNA.

Messenger RNA was purified from total RNA using an Poly(A)Pure kit (Ambion, Austin TX), following the manufacturer's instructions. A reverse transcription reaction was used to synthesize cDNA from the mRNA template, using either the Stratagene (La Jolla, CA) or Gibco BRL (Gaithersburg, MD) cDNA cloning kits. For the Stratagene library, the cDNAs were subcloned into bacteriophage at EcoR1/XhoI site by ligating the arms using the Gigapack III Gold kit (Stratagene, La Jolla, CA), following the manufacturer's instructions. For the Gibco BRL library, the cDNAs were subcloned into a tobamoviral vector that contained a fusion of TMV-U1 and TMV-U5 at the *NotI*/XhoI sites.

EXAMPLE 18

Rapid isolation of cDNAs encoding human ADP-ribosylation factor

Libraries containing full-length human cDNAs from organisms such as brain, liver, breast, lung, etc. are obtained from public and private sources or prepared from human mRNAs. The cDNAs are inserted in viral vectors or in small subcloning vectors such as pBluescript (Stratagene), pUC18, M13, or pBR322. Transformed bacteria (*E. coli*) are then plated on large petri plates or bioassay plates containing the appropriate media and antibiotic. Individual clones are selected using a robotic colony picker and arrayed into 96 well microtiter plates. The cultures are incubated at 37°C until the transformed cells reach log phase. Aliquots are removed to prepare glycerol stocks for long term storage at -80°C. The remainder of the culture is used to inoculate an additional 96 well microtiter plate containing selective media and grown overnight. DNAs are isolated from the cultures and stored at -20°C. Using a robotic unit such as the Qbot (Genetix), the *E. coli* transformants or DNAs are rearrayed at high density on nylon or nitrocellulose filters or glass slides. Full-length cDNAs encoding ARFs from human brain, liver, breast, lung, etc. are isolated

by screening the various filters or slides by hybridization with a ³²P-labeled or fluorescent 740 AT #2441 *NotI* insert.

EXAMPLE 19

Construction of a viral vector containing human cDNAs.

5 An ARF5 clone containing nucleic acid inserts from a human brain cDNA library (Bobak *et al.*, *Proc. Natl. Acad. Su.* USA 86:6101-6105 (1989)) was isolated by polymerase chain reaction (PCR) using the following oligonucleotides: HARFMIA, 5' TAC CTA GGG CAA TAT CTT TGG AAA CCT TCT CAA G 3' (upstream)(SEQ ID NO: 48), HARFK181X, 5' CGC TCG AGT CAC TTC TTG TTT TTG AGC TGA TTG GCC AG 3' 10 (downstream)(SEQ ID NO: 49). The vent polymerase in the reaction was inactivated using phenol/chloroform. The PCR product are directly cloned into the *XhoI*, *AvrII* site TTO1A.

EXAMPLE 20

Identification of human nucleotide sequences involved in the regulation of plant growth by cytoplasmic inhibition of gene expression using viral derived RNA containing human 15 nucleotide sequences.

A human brain cDNA library are obtained from public and private sources or prepared from human mRNAs. The cDNAs are inserted in viral rectors or in small subcloning vectors and the cDNA inserts are isolated from the cloning vectors with appropriate enzymes, modified, and *NotI* linkers are attached to the cDNA blunt ends. The 20 human cDNA inserts are subcloned into the *NotI* site of pBS740. *E. coli* C600 competent cells are transformed with the pBS740 sublibrary and colonies containing human cDNA sequences are selected on LB Amp 50 ug/ml. DNAs containing the viral human brain cDNA library are purified from the transformed colonies and used to make infectious RNAs that are directly applied to plants. One to three weeks post transfection, the plants 25 developing severe stunting phenotypes are identified and their corresponding viral vector inserts are characterized by nucleic acid sequencing.

Humanizing plant homolog for expression of plant derived human protein

In order to obtain the corresponding plant cDNAs, the human clones responsible for causing changes in the transfected plant phenotype (for example, stunting) are used as

probes. Full-length plant cDNAs are isolated by hybridizing filters or slides containing *N. benthamiana* cDNAs with ³²P-labeled or fluorescent human cDNA insert probes. The positive plant clones are characterized by nucleic acid sequencing and compared with their human homologs. Plant codons that encode for different amino acids are changed by site directed mutagenesis to codons that encode for the same amino acids as their human homologs. The resulting "humanized" plant cDNAs encode an identical protein as the human clone. The "humanized" plant clones are used to produce human proteins in either transfected or transgenic plants by standard techniques. Because the "humanized" cDNA is from a plant origin, it is optimal for expression in plants.

10

EXAMPLE 21

Identification of *Arabidopsis* nucleotide sequences involved in the regulation of plant development and comparison with octopus rhodopsin cDNA.

This example again demonstrates that an episomal RNA viral vector can be used to deliberately manipulate a signal transduction pathway in plants, and identify nucleic acid sequences that involved the regulation of plant development.

15

A partial *Arabidopsis thaliana* cDNA library was placed under the transcriptional control of a tobamovirus subgenomic promoter in a RNA viral vector. Colonies from transformed *E. coli* were automatically picked using a Flexys robot and transferred to a 96 well flat bottom block containing terrific broth (TB) Amp 50 ug/ml. Approximately 2000 plasmid DNAs were isolated from overnight cultures using a BioRobot and infectious RNAs from 430 independent clones were directly applied to plants. One to two weeks after inoculation, transfected *Nicotiana benthamiana* plants were visually monitored for changes in growth rates, morphology, and color. One set of plants transfected with 740 AT #909 (FIGURE 21) developed a white phenotype on the infected leaf tissue. DNA sequence analysis revealed that this clone contained an *Arabidopsis* ribosomal protein L19 open reading frame (ORF) in the positive sense orientation.

20

25

DNA sequencing and computer analysis.

30

The bp *Not*I fragment of 740 AT #909 containing the ribosomal protein L19 cDNA was characterized. The nucleotide sequencing of 740 AT #909 was carried

out by dideoxy termination using double stranded templates (Sanger *et al.*, 1977).

Nucleotide sequence analysis and amino acid sequence comparisons were performed using DNA Strider, PCGENE and NCBI Blast programs. FIGURE 22 shows nucleotide alignment of 740 AT #909 (SEQ ID NO: 50) to human S5 6985 ribosomal protein L19

- 5 cDNA (SEQ ID NO: 51) FIGURE 23 shows the amino acid sequence alignment of 740 AT #909 to human P14118 60S ribosomal protein L19. Table 4 shows the 740 AT #909 nucleotide sequence comparison to plant drosophila, yeast, and human: 63-79% identities and positives are shown. Table 5 show the 740 AT #909 amino acid comparison to plant, human, mouse, yeast, and insect L19 ribosomal protein: 65-88% identities and 80-92% positives are shown.
- 10

Table 4. 740 AT #909 Nucleotide sequence comparison

<u>Clone</u>	<u>Score</u>	<u>Pvalue</u>	<u>Identities</u>	<u>Positives</u>
<i>A. tabacum</i> L19 mRNA Z31720	1389 (383.8 bits)	1.20E-107	349/438 (79%)	349/438 (79%)
<i>D. melanogaster</i> L19 mRNA L32181	970 (268.0 bits)	4.50E-73	298/428 (69%)	298/428 (69%)
<i>S. pombe</i> L19 mRNA AB01004	779 (215.3 bits)	1.30E-55	275/424 (64%)	275/424 (64%)
<i>D. melanogaster</i> rpL19 gene X74776	780 (215.5 bits)	2.10E-55	240/345 (69%)	240/345 (69%)
<i>M. musculus</i> L19 mRNA M62952	768 (212.2 bits)	1.60E-54	280/438 (63%)	280/438 (63%)
<i>D. discoideum</i> L19 mRNA L27657	759 (209.7 bits)	7.90E-54	279/438 (63%)	279/438 (63%)
Human breast cancer L19 mRNA S56985	732 (202.3 bits)	2.60E-51	276/438 (63%)	276/438 (63%)

Table 5 740 AT #909 Nucleotide sequence comparison

<u>Clone</u>	<u>Score</u>	<u>Pvalue</u>	<u>Identities</u>	<u>Positives</u>
Human L19 ribosomal protein P14118	556 (255.8 bits)	6.50E-72	101/156 (69%)	124/146 (84%)
Mouse L19 ribosomal protein P22908	556 (255.8 bits)	6.50E-72	101/146 (69%)	124/146 (84%)
<i>A. thaliana</i> L19 ribosomal protein P49693	542 (249.3 bits)	8.90E-70	105/118 (88%)	109/118 (92%)
<i>D. discoideum</i> L19 ribosomal protein P14329	537 (247.0 bits)	2.90E-69	99/146 (67%)	121/146 (82%)
<i>D. melanogaster</i> L19 ribosomal protein P36241	530 (243.8 bits)	2.50E-68	99/146 (67%)	118/146 (80%)
<i>S. pombe</i> L19 ribosomal protein O42699	526 (242.0 bits)	9.70E-68	98/140 (70%)	116/140 (82%)
<i>C. elegans</i> L19 ribosomal protein O02639	503 (231.4 bits)	1.40E-64	91/139 (65%)	116/139 (83%)

EXAMPLE 22

Novel requirements for production of infectious viral vector *in vitro* derived RNA transcripts.

This example demonstrates the production of highly infectious viral vector
5 transcripts containing 5' nucleotides with reference to the virus vector.

Construction of a library of subgenomic cDNA clones of TMV and BMV has
been described in Dawson *et al.*, *Proc. Natl. Acad. Sci. USA* 83:1832-1836 (1986) and
Ahlquist *et al.*, *Proc. Natl. Acad. Sci. USA* 81:7066-7070 (1984). Nucleotides were
added between the transcriptional start site of the promoter for *in vitro* transcription, in
10 this case T7, and the start of the cDNA of TMV in order to maximize transcription
product yield and possibly obviate the need to cap virus transcripts to insure infectivity.
The relevant sequence is the T7 promoter ...TATAG[^]TATTTT (SEQ ID NO: 52) where
the ^ indicates the base preceding is the start site for transcription and the bold letter is
the first base of the TMV cDNA. Three approaches were taken: 1) addition of G, GG or
15 GGG between the start site of transcription and the TMV cDNA (... TATAGGTATTT,
SEQ ID NO: 53, and associated sequences); 2) addition of G and a random base (GN or
N2) or a G and two random bases (GNN or N3) between the start site of transcription
and the TMV cDNA (...TATAGNTATTT, SEQ ID NO: 54, and associated sequences),
and the addition of a GT and a single random base between the start site of transcription
20 and the TMV cDNA (...TATAGTNGTATTT, SEQ ID NO: 55 and associated
sequences). The use of random bases was based on the hypothesis that a particular base
may be best suited for an additional nucleotide attached to the cDNA, since it will be
complementary to the normal nontemplated base incorporated at the 3'-end of the TMV
(-) strand RNA. This allows for more ready mis-initiation and restoration of wild type
25 sequence. The GTN would allow the mimicking of two potential sites for initiation, the
added and the native sequence, and facilitate more ready mis-initiation of transcription
in vivo to restore the native TMV cDNA sequence. Approaches included cloning GFP
expressing TMV vector sequences into vectors containing extra G, GG or GGG bases
using standard molecular biology techniques. Likewise, full length PCR of TMV
30 expression clone 1056 was done to add N2, N3 and GTN bases between the T7

promoter and the TMV cDNA. Subsequently, these PCR products were cloned into pUC based vectors. Capped and uncapped transcripts were made *in vitro* and inoculated to tobacco protoplasts or *Nicotiana benthamiana* plants, wild type and 30k expressing transgenics. The results are that an extra G, ... TATAGGTATTTT, SEQ ID NO: 56, or
5 a GTC, ... TATAGTCGTATTTT, SEQ ID NO: 57, were found to be well tolerated as additional 5' nucleotides on the 5' of TMV vector RNA transcripts and were quite infectious on both plant types and protoplasts as capped or non-capped transcripts. Other sequences may be screened to find other options. Clearly, infectious transcripts may be derived with extra 5' nucleotides.

10 Other derivatives based on the putative mechanistic function of the GTN strategy that yielded the GTC functional vector are to use multiple GTN motifs preceeding the 5' most nt of the virus cDNA or the duplication of larger regions of the 5'-end of the TMV genome. For example: TATA^GTNGTNGTATT, SEQ ID NO: 58, or TATA^GTNGTNGTNGTNGTATT, SEQ ID NO: 185, or
15 TATA^GTATTTGTATTT, SEQ ID NO: 59. In this manner the replication mediated repair mechanism may be potentiated by the use of multiple recognition sequences at the 5'-end of transcribed RNA. The replicated progeny may exhibit the results of reversion events that would yield the wild type virus 5' virus sequence, but may include portions or entire sets of introduced additional base sequences. This strategy can be
20 applied to a range of RNA viruses or RNA viral vectors of various genetic arrangements derived from wild type virus genome. This would require the use of sequences particular to that of the virus used as a vector.

EXAMPLE 23

Infectivity of uncapped transcripts.

25 Two TMV-based virus expression vectors were initially used in these studies pBTI 1056 which contains the T7 promoter followed directly by the virus cDNA sequence (...TATAGTATT...), and pBTI SBS60-29 which contains the T7 promoter (underlined) followed by an extra guanine residue then the virus cDNA sequence (...TATAGGTATT...). Both expression vectors express the cycle 3 shuffled green
30 fluorescent protein (GFPc3) in localized infection sites and systemically infected tissue

of infected plants. Transcriptions of each plasmid were carried out in the absence of cap analogue (uncapped) or in the presence of 8-fold greater concentration of RNA cap analogue than rGTP (capped). Transcriptions were mixed with abrasive and inoculated on expanded older leaves of a wild type *Nicotiana benthamiana* (Nb) plant and a Nb
5 plant expressing a TMV UI 30k movement protein transgene (Nb 30K). Four days post inoculation (dpi), long wave UV light was used to judge the number of infection sites on the inoculated leaves of the plants. Systemic, noninoculated tissues, were monitored from 4 dpi on for appearance of systemic infection indicating vascular movement of the inoculated virus. Table 6 shows data from one representative experiment.

Table 6

Construct	Local infection sites		Systemic Infection	
	Nb	Nb 30K	Nb	Nb 30K
pBTI1056				
15 Capped	5	6	yes	yes
Uncapped	0	5	no	yes
PBTI SBS60-29				
20 Capped	6	6	yes	yes
Uncapped	1	5	yes	yes

Nicotiana tabacum protoplasts were infected with either capped or uncapped transcriptions (as described above) of pBTI SBS60 which contains the T7 promoter followed directly by the virus cDNA sequence (TATAGTATT...). This expression
25 vector also expresses the GFPc3 gene in infected cells and tissues. *Nicotiana tabacum* protoplasts were transfected with 1 mcl of each transcriptions. Approximately 36 hours post infection transfected protoplasts were viewed under UV illumination and cells showing GFPc3 expression. Approximately 80% cells transfected with the capped PBTI SBS60 transcripts showed GFP expression while 5% of cells transfected with
30 uncapped transcripts showed GFP expression. These experiments were repeated with higher amounts of uncapped inoculum. In this case a higher proportion of cells, >30% were found to be infected at this time with uncapped transcripts, where >90% of cells infected with greater amounts of capped transcripts were scored infected.

These results indicate that, contrary to the practiced art in scientific literature and in issued patents (Ahlquist *et al.*, U.S. Patent No. 5,466,788), uncapped transcripts for virus expression vectors are infective on both plants and in plant cells, however with much lower specific infectivity. Therefore, capping is not a prerequisite for establishing an infection of a virus expression vector in plants; capping just increases the efficiency of infection. This reduced efficiency can be overcome, to some extent, by providing excess *in vitro* transcription product in an infection reaction for plants or plant cells.

The expression of the 30K movement protein of TMV in transgenic plants also has the unexpected effect of equalizing the relative specific infectivity of uncapped versus capped transcripts. The mechanism behind this effect is not fully understood, but could arise from the RNA binding activity of the movement protein stabilizing the uncapped transcript in infected cells from prereplication cytosolic degradation.

Extra guanine residues located between the T7 promoter and the first base of a virus cDNA lead to increased amount of RNA transcript as predicted by previous work with phage polymerases. These polymerases tend to initiate more efficiently at ...TATAGG or ...TATAGGG than ...TATAG. This has an indirect effect on the relative infectivity of uncapped transcripts in that greater amounts are synthesized per reaction resulting in enhanced infectivity.

Data concerning cap dependent transcription of pBTI1056 GTN#28.

TMV-based virus expression vector pBTI 1056 GTN#28 which contains the T7 promoter (underlined) followed GTC bases (bold) then the virus cDNA sequence (...TATAG**GTC**GTATT, SEQ ID NO: 60). This expression vector expresses the cycle 3 shuffled green fluorescent protein (GFPc3) in localized infection sites and systemically infected tissue of infected plants. This vector was transcribed *in vitro* in the presence (capped) and absence (uncapped) of cap analogue. Transcriptions were mixed with abrasive and inoculated on expanded older leaves of a wild type *Nicotiana benthamiana* (Nb) plant and a Nb plant expressing a TMV U1 30k movement protein transgene (Nb 30K). Four days post inoculation (dpi) long wave UV light was used to judge the number of infection sites on the inoculated leaves of the plants. Systemic, non-inoculated tissues, were monitored from 4 dpi on for appearance of systemic infection

indicating vascular movement of the inoculated virus. Table 7 shows data from two representative experiments at 11 dpi.

5

Table 7

	Construct	Local infection sites		Systemic Infection	
		Nb	Nb 30K	Nb	Nb 30K
	Experiment 1				
	pBTI1056 GTN#28				
10	Capped	18	25	yes	yes
	Uncapped	2	4	yes	yes
	Experiment 2				
15	pBTI1056 GTN#28				
	Capped	8	12	yes	yes
	Uncapped	3	7	yes	yes

20

These data further support the claims concerning the utility of uncapped transcripts to initiate infections by plant virus expression vectors and further demonstrates that the introduction of extra, non-viral nucleotides at the 5'-end of *in vitro* transcripts does not preclude infectivity of uncapped transcripts.

25

Although the invention has been described with reference to the presently preferred embodiments, it should be understood that various modifications can be made without departing from the spirit of the invention.

CLAIMS

What is claimed is:

1. A method of changing the phenotype or biochemistry of a plant, comprising:
 - (a) expressing transiently a nucleic acid sequence from a donor organism
5 selected from the group consisting of *Monera*, *Protista*, *Fungi*, and *Animalia*, in a positive sense orientation in a host plant;
 - (b) determining one or more phenotypic or biochemical changes in said host plant.
2. A method of determining a change in phenotype or biochemistry in a plant due
10 to a cytoplasmic expression of a nucleic acid in a positive sense orientation, comprising:
 - (a) expressing transiently a nucleic acid sequence from a donor organism
selected from the group consisting of *Monera*, *Protista*, *Fungi*, and *Animalia*, in a positive sense orientation in a host plant;
 - (b) determining one or more biochemical or phenotypic changes in said host
15 plant; and
 - (c) correlating said one or more biochemical or phenotypic changes to a host plant that is uninfected.
3. The method according to Claim 2, further comprises the step of correlating said
one or more biochemical or phenotypic changes to a host plant that is infected with a
20 viral vector that contains a known nucleic acid sequence of like size in a positive sense orientation, wherein said known nucleic acid sequence has similar size but is different in sequence from said nucleic acid sequence in (a).
4. A method of determining the presence of a trait in a plant, comprising:
 - (a) expressing transiently a nucleic acid sequence from a donor organism
25 selected from the group consisting of *Monera*, *Protista*, *Fungi*, and *Animalia*, in a positive sense orientation in a host plant;
 - (b) determining one or more biochemical or phenotypic changes in said host plant;

(c) correlating said one or more biochemical or phenotypic changes to a host plant that is uninfected; and

(d) identifying a trait present in said uninfected host plant.

5. The method according to Claim 4, further comprises the step of correlating said one or more biochemical or phenotypic changes to a host plant that is infected with a viral vector that contains a known nucleic acid sequence in a positive sense orientation, wherein said known nucleic acid sequence has similar size but is different in sequence from said nucleic acid sequence in (a).

6. A method of determining the presence of a trait in a plant, comprising:

10 (a) expressing transiently nucleic acid sequence from a donor organism selected from the group consisting of *Monera*, *Protoctista*, *Fungi*, and *Animalia*, in a positive sense orientation in a host plant;

(b) determining one or more biochemical or, phenotypic changes in said host plant;

15 (c) correlating said one or more biochemical or phenotypic changes to a host plant that is uninfected; and

(d) identifying a trait present in said infected host plant.

7. The method according to Claim 6, further comprises the step of correlating said one or more biochemical or phenotypic changes to a host plant that is infected with a viral vector that contains a known nucleic acid sequence but in a positive sense orientation, wherein said known nucleic acid sequence has similar size but is different in sequence from said nucleic acid sequence in (a).

8. The method according to Claim 1, 2, 4, or 6, wherein said nuclei acid sequence from said donor has not been identified.

25 9. The method according to Claim 1, 2, 4, or 6, wherein said host plant is selected from the group consisting of food crops, seed crops, oil crops, ornamental crops and forestry.

10. The method according to Claim 9, wherein said host plant is *Nicotiana*.

11. The method according to Claim 10, wherein said host plant is *Nicotiana benthamina* or *Nicotiana cleavlandii*.
12. The method according to Claim 1, 2, 4, or 6, wherein said nucleic acid sequence is derived from a library of cDNAs, genomic DNAs, or a pool of mRNAs, which
5 represents all or part of the donor organism genome.
13. The method according to Claim 12, further comprising the step of cloning said nucleic acid sequence into a plant viral vector.
14. The method according to Claim 13, wherein the plant viral vector genome is capped or uncapped.
- 10 15. The method according to Claim 13, further comprising the step of infecting said host plant with a recombinant viral nucleic acid comprising said nucleic acid sequence.
16. The method according to Claim 15, wherein said recombinant viral nucleic acid further comprises a native plant viral subgenomic promoter and a plant viral coat protein coding sequence.
- 15 17. The method according to Claim 16, wherein said recombinant viral nucleic acid further comprises a non-native plant viral subgenomic promoter, said native plant viral subgenomic promoter initiates transcription of said plant viral coat protein sequence and said non-native plant viral subgenomic promoter initiates transcription of said nucleic acid sequence.
- 20 18. The method according to Claim 13, wherein a plus sense RNA is produced in the cytoplasm of said host plant, and said plus sense RNA results in overexpression of a protein in said host plant.
19. The method according to Claim 13, wherein a plus sense RNA is produced in the cytoplasm of said host plant, and said plus sense RNA results in an enhanced or
25 reduced expression of an endogenous gene in said host plant.

20. The method according to Claim 18 or 19 wherein said nucleic acid sequence encodes a GTP binding protein.
21. The method according to Claim 19, wherein said plus sense RNA results in a reduced expression of an endogenous gene in said host plant.
- 5 22. The method according to Claim 21, wherein said nucleic acid sequence does not contain a start codon.
23. The method according to Claim 21, wherein said nucleic acid encodes an untranslated region.
24. The method according to Claim 13, wherein said recombinant viral nucleic acids
10 are derived from a plant virus.
25. The method according to Claim 24, wherein said plant virus is selected from the group consisting of a potyvirus, a tobamovirus, a bromovirus, and a geminivirus.
26. The method according to Claim 25, wherein said potyvirus is a rice necrosis virus.
15
27. The method according to Claim 1, 2, 4 or 6, wherein said phenotypic changes are changes in growth rates, morphology, or color.
28. A method of determining the presence of a trait in a plant, comprising:
(a) expressing transiently a nucleic acid sequence of a donor organism
20 selected from the group consisting of *Monera*, *Protista*, *Fungi*, and *Animalia*, in a positive sense orientation in a host plant;
(b) determining phenotypic or biochemical changes in said host plant; and
(c) correlating said expression with said phenotypic or biochemical changes,
wherein said nucleic acid sequence comprising a GTP binding protein open reading
25 frame having a positive sense orientation.
29. The method according to Claim 28, wherein said GTP binding protein is

selected from the group consisting of *rab* family, and ADP-ribosylation factor family.

30. A method for identifying a nucleic acid sequence in a donor organism selected from the group consisting of *Monera*, *Protista*, *Fungi*, and *Animalia*, having the same function as that in a host plant, said method comprising the steps of:

- 5 (a) preparing a library of cDNAs, genomic DNAs, or a pool of mRNAs of said donor organism,
- (b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,
- (c) infecting each said host plant with one of said recombinant viral nucleic
10 acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,
- (d) growing said infected host plant,
- (e) determining one or more changes in said host plant,
- (f) identifying said recombinant viral nucleic acid that results in changes in
15 said host plant, and
- (g) determining the sequence of said nucleic acid insert in said recombinant viral nucleic acid, and
- (h) determining the sequence of an entire open reading frame of said donor from which said nucleic acid insert is derived.

20 31. The method according to Claim 30, wherein said donor organism is human.

32. A method for identifying a human nucleic acid sequence, said method comprising the steps of:

- (a) preparing a human cDNA library,
- (b) constructing recombinant viral nucleic acids comprising a nucleic acid
25 insert derived from said library,
- (c) infecting a host plant with one of said recombinant viral nucleic acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,
- (d) growing said infected host plant,

- (e) determining one or more changes in said host plant,
(f) identifying said recombinant viral nucleic acid that results in said changes in said host plant,
(g) determining the sequence of said nucleic acid insert in said recombinant viral nucleic acid, and
5 (h) determining the sequence of an entire open reading frame in said human from which said nucleic acid insert is derived.
33. A method for isolating human cDNAs, said method comprising the steps of:
10 (a) obtaining a cDNA library from a human organism,
(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,
(c) infecting a host plant with said recombinant viral nucleic acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,
15 (d) growing said infected host plant,
(e) determining one or more changes in said host plant,
(f) identifying said recombinant viral nucleic acid that results in changes in said host plant,
(g) sequencing and labeling said nucleic acid insert in said recombinant viral
20 nucleic acid of (f),
(h) probing filters or slides containing full-length human cDNAs with said labeled nucleic acid insert, and
(i) isolating said full-length human cDNA that hybridizes to said labeled nucleic acid insert.
- 25 34. A method for humanizing a plant cDNA, said method comprising the steps of:
(a) obtaining a cDNA library from a human organism,
(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,
(c) infecting a host plant with said recombinant viral nucleic acids, and
30 expressing transiently said nucleic acid in a positive sense orientation in said host plant,

- (d) growing said infected host plant,
- (e) determining one or more changes in said host plant,
- (f) identifying said recombinant viral nucleic acid that results in changes in said host plant,
- 5 (g) sequencing and labeling said nucleic acid insert in said recombinant viral nucleic acid of (f),
- (h) probing filters or slides containing full-length human cDNAs or full-length plant cDNAs with said labeled nucleic acid insert,
- (i) isolating said full-length human cDNA and plant cDNA that hybridize to
- 10 said labeled nucleic acid insert,
- (j) comparing the amino acid sequences derived from said human cDNA and said plant cDNA, and
- (k) changing said plant cDNA sequence so that it encodes the same amino acid sequence as said human cDNA encodes.
- 15 35. The method according to Claim 32, 33, or 34 wherein said nucleic acid sequence encodes a protein that regulates growth of cells or organisms in human.
36. The method according to Claim 35, wherein said protein is a L19 ribosomal protein, a GTP binding protein, or a S18 ribosomal protein.
37. The method according to Claim 32, 33, or 34 wherein said nucleic acid sequence
- 20 encodes a protein that regulates a development fate in human.
38. The method according to Claim 37, wherein said protein belongs to a rhodopsin family.
39. A method of increasing yield of a grain crop, said method comprising expressing transiently a nucleic acid sequence of a non-plant organism in a positive sense
- 25 orientation in said grain crop, wherein said expressing results in stunted growth and increased seed production of said grain crop.
40. The method according to Claim 39, further comprising the step of cloning said nucleic acid sequence into a plant viral vector.

41. The method according to Claim 40, further comprising infecting said grain crop with a recombinant viral nucleic acid comprising said nucleic acid sequence.

42. The method according to Claim 41, wherein said nucleic acid comprises a GTP binding protein open reading frame having a positive sense orientation.

5 43. The method according to Claim 39, wherein said grain crop is rice.

44. The method according to Claim 40, wherein said plant viral vector is derived from a virus selected from the group consisting of a Brome Mosaic virus, a Rice Necrosis virus, and a geminivirus.

45. A method of compiling a positive sense functional gene profile of an organism
10 comprising:

- (a) preparing a vector library of DNA or RNA sequences from a donor organism, each sequence being in a positive sense orientation;
 - (b) infecting a plant host with a vector;
 - (c) transiently expressing the donor DNA or RNA sequence in said growing
15 plant host;
 - (d) determining one or more phenotypic or biochemical changes in said plant host;
 - (e) identifying an associated trait where a phenotypic or biochemical change occurs;
 - 20 (f) identifying a donor gene associated with the trait;
 - (g) identifying a plant host gene, which is associated with the trait; and
- repeating steps b) – g) until a positive sense functional gene profile of said plant host and/or of said donor organism is compiled.

ABSTRACT

5 The present invention provides a method of compiling a positive sense
functional gene profile of an organism, a method of changing the phenotype or
biochemistry of an organism, a method of determining a change in phenotype or
10 biochemistry of an organism, and a method of determining the presence of a trait in an
organism. The methods comprise expressing transiently a nucleic acid sequence of a
donor organism into a host plant to affect phenotypic or biochemical changes in the host
organism. A viral vector functional genomic screen has been developed to identify
nucleotide sequences in transfected plants by enhancing or suppressing an endogenous
15 gene expression in a positive sense mechanism, or by overexpressing a new protein.
Once the presence of a trait in a plant is identified by phenotypic or biochemical
changes in the host plant, the nucleic acid insert in the cDNA clone or in the vector that
results in the changes is then sequenced. The present invention provides a method for
discovering new gene and its function in a donor organism such as human by
20 transfected a nucleic acid sequence of the donor organism into a host organism in a
positive sense.

Sedimentation		Gel Permeation Chromatography		Intrinsic Viscosity		Oxidation		Thermal Stability		Solubility		Molecular Weight		Polydispersity	
Sample	Value	Sample	Value	Sample	Value	Sample	Value	Sample	Value	Sample	Value	Sample	Value	Sample	Value
1	1.2	1	1.2	1	1.2	1	1.2	1	1.2	1	1.2	1	1.2	1	1.2
2	1.5	2	1.5	2	1.5	2	1.5	2	1.5	2	1.5	2	1.5	2	1.5
3	1.8	3	1.8	3	1.8	3	1.8	3	1.8	3	1.8	3	1.8	3	1.8
4	2.1	4	2.1	4	2.1	4	2.1	4	2.1	4	2.1	4	2.1	4	2.1
5	2.4	5	2.4	5	2.4	5	2.4	5	2.4	5	2.4	5	2.4	5	2.4
6	2.7	6	2.7	6	2.7	6	2.7	6	2.7	6	2.7	6	2.7	6	2.7
7	3.0	7	3.0	7	3.0	7	3.0	7	3.0	7	3.0	7	3.0	7	3.0
8	3.3	8	3.3	8	3.3	8	3.3	8	3.3	8	3.3	8	3.3	8	3.3
9	3.6	9	3.6	9	3.6	9	3.6	9	3.6	9	3.6	9	3.6	9	3.6
10	3.9	10	3.9	10	3.9	10	3.9	10	3.9	10	3.9	10	3.9	10	3.9
11	4.2	11	4.2	11	4.2	11	4.2	11	4.2	11	4.2	11	4.2	11	4.2
12	4.5	12	4.5	12	4.5	12	4.5	12	4.5	12	4.5	12	4.5	12	4.5
13	4.8	13	4.8	13	4.8	13	4.8	13	4.8	13	4.8	13	4.8	13	4.8
14	5.1	14	5.1	14	5.1	14	5.1	14	5.1	14	5.1	14	5.1	14	5.1
15	5.4	15	5.4	15	5.4	15	5.4	15	5.4	15	5.4	15	5.4	15	5.4
16	5.7	16	5.7	16	5.7	16	5.7	16	5.7	16	5.7	16	5.7	16	5.7
17	6.0	17	6.0	17	6.0	17	6.0	17	6.0	17	6.0	17	6.0	17	6.0
18	6.3	18	6.3	18	6.3	18	6.3	18	6.3	18	6.3	18	6.3	18	6.3
19	6.6	19	6.6	19	6.6	19	6.6	19	6.6	19	6.6	19	6.6	19	6.6
20	6.9	20	6.9	20	6.9	20	6.9	20	6.9	20	6.9	20	6.9	20	6.9
21	7.2	21	7.2	21	7.2	21	7.2	21	7.2	21	7.2	21	7.2	21	7.2
22	7.5	22	7.5	22	7.5	22	7.5	22	7.5	22	7.5	22	7.5	22	7.5
23	7.8	23	7.8	23	7.8	23	7.8	23	7.8	23	7.8	23	7.8	23	7.8
24	8.1	24	8.1	24	8.1	24	8.1	24	8.1	24	8.1	24	8.1	24	8.1
25	8.4	25	8.4	25	8.4	25	8.4	25	8.4	25	8.4	25	8.4	25	8.4
26	8.7	26	8.7	26	8.7	26	8.7	26	8.7	26	8.7	26	8.7	26	8.7
27	9.0	27	9.0	27	9.0	27	9.0	27	9.0	27	9.0	27	9.0	27	9.0
28	9.3	28	9.3	28	9.3	28									

The diagram illustrates the circular plasmid pBR322, which is 11.6 kb in size. The plasmid contains the TTO1/PSY⁺ gene, represented by a thick black arc. Key features include:

- Restriction Sites:** ClaI, XhoI, BamHI, and KpnI sites are marked around the plasmid.
- Genetic Elements:** A Tc^r resistance gene is present, along with two TMV RNA insertion sites at positions +7866 and +1.
- Gene Structure:** The TTO1/PSY⁺ gene is divided into segments labeled 30K, 183/54K, and 126K.
- Inset:** A detailed view of the 126K region shows a 68 nt spacer followed by an SP6 promoter.

• • •

66T2.2" 00665560

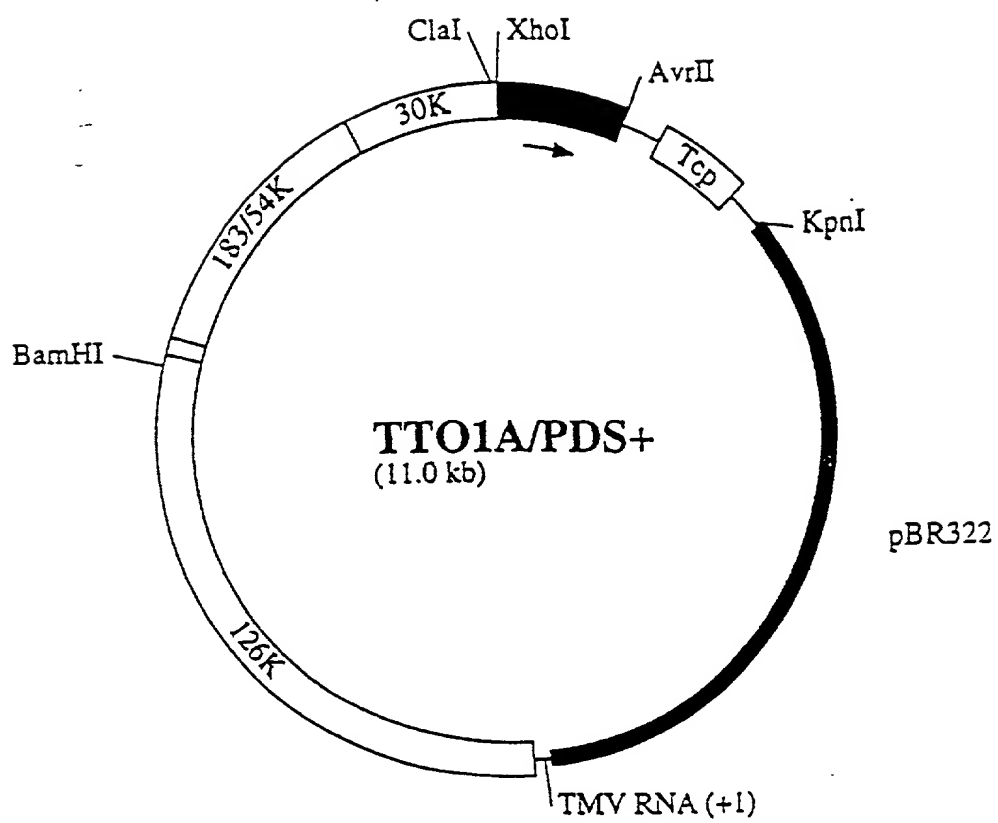


Figure 2

.tsp XhoI Start codon
 GTTTAAATACGCTCGAGTGCAGC ATG GAA ACC CTT CTA AAG CCT TTT CCA TCT CCT TTA CTT
 Met Glu Thr Leu Leu Lys Pro Phe Pro Ser Pro Leu Leu

Transit peptide of capsanthin-capsorubin synthase
 TCC ATT CCT ACT CCT AAC ATG TAT AGT TTC AAA CAC AAC TTC ACT TTT
 Ser Ile Pro Thr Pro Asn Met Tyr Ser Phe Lys His Asn Ser Thr Phe

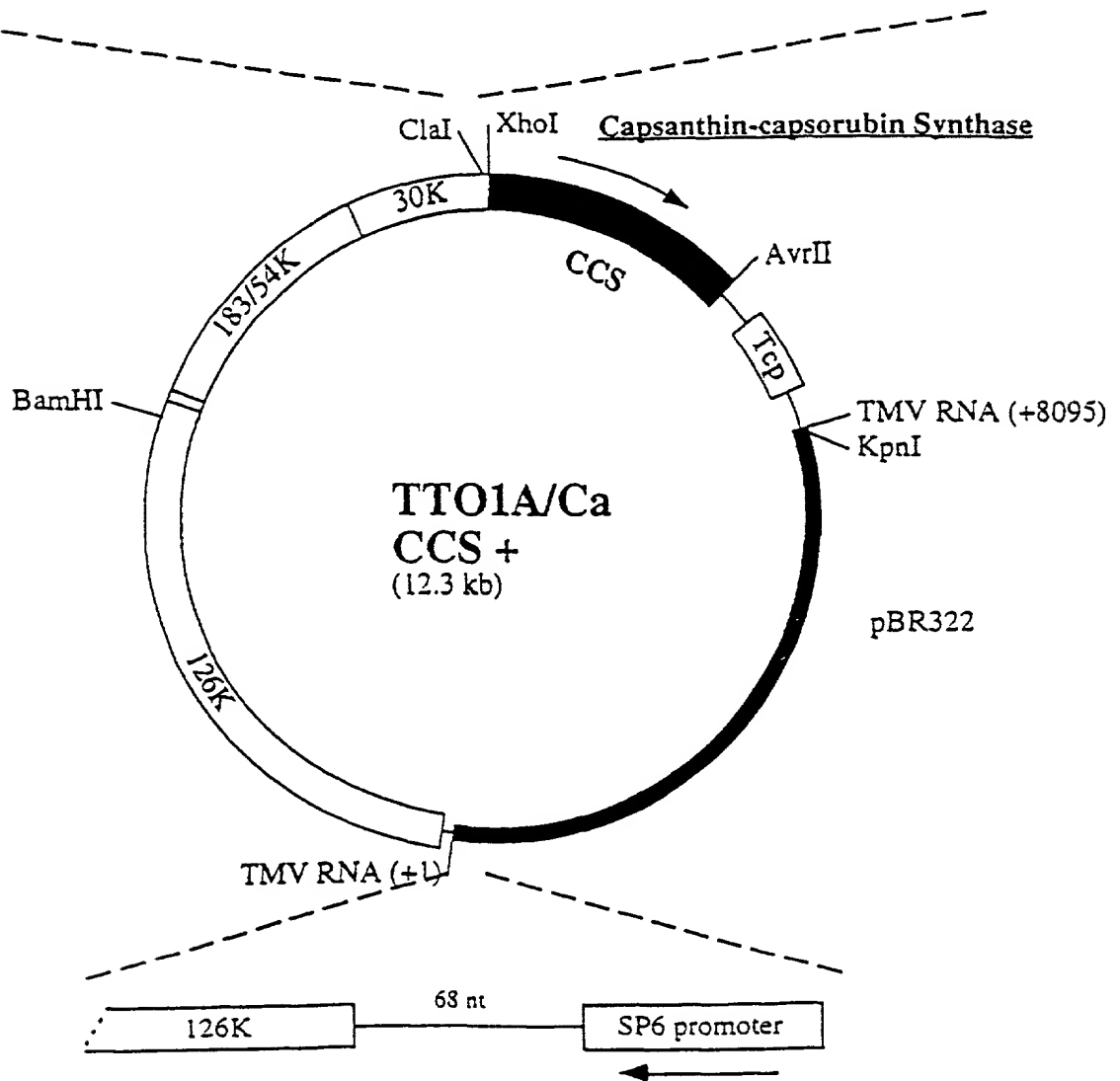


Figure 3

Figure 4

.tsp XhoI Start codon

GT	TTT	A	A	T	A	T	A	C	G	T	C	G	A	G	C
Met	Ala	Ser	Ser	Val	Leu	Ser	Ser	Ala	Ala	Val	Ala	Thr	Arg		

RUBISCO SSU Chloroplast Transit Peptide (*N. tabacum*)

AGC AAT GTT GCT CAA GCT AAC ATG GTT GCA CCT TTC ACT GGC CTT

Ser Asn Val Ala Gln Ala Asn Met Val Ala Pro Phe Thr Gly Leu

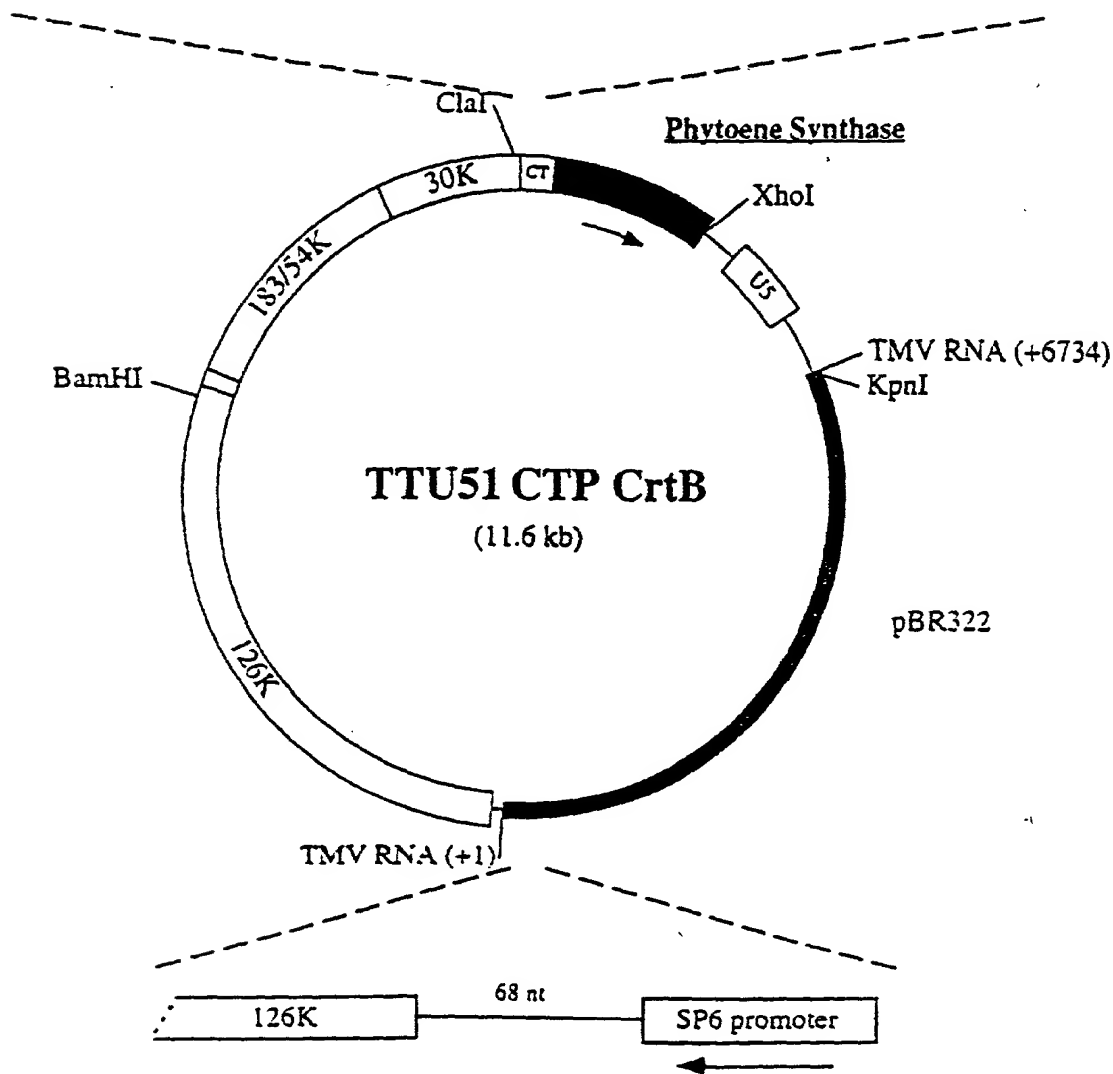


Figure 5

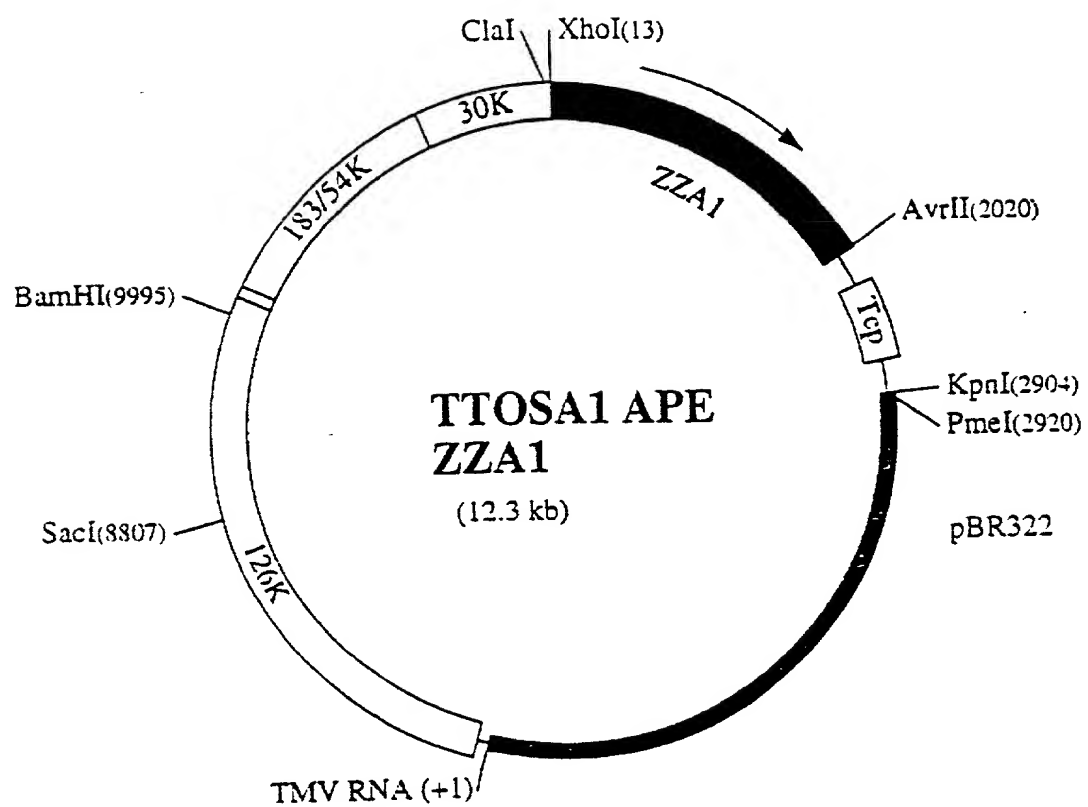


Figure 6

09369300 073199
66T970 00055520

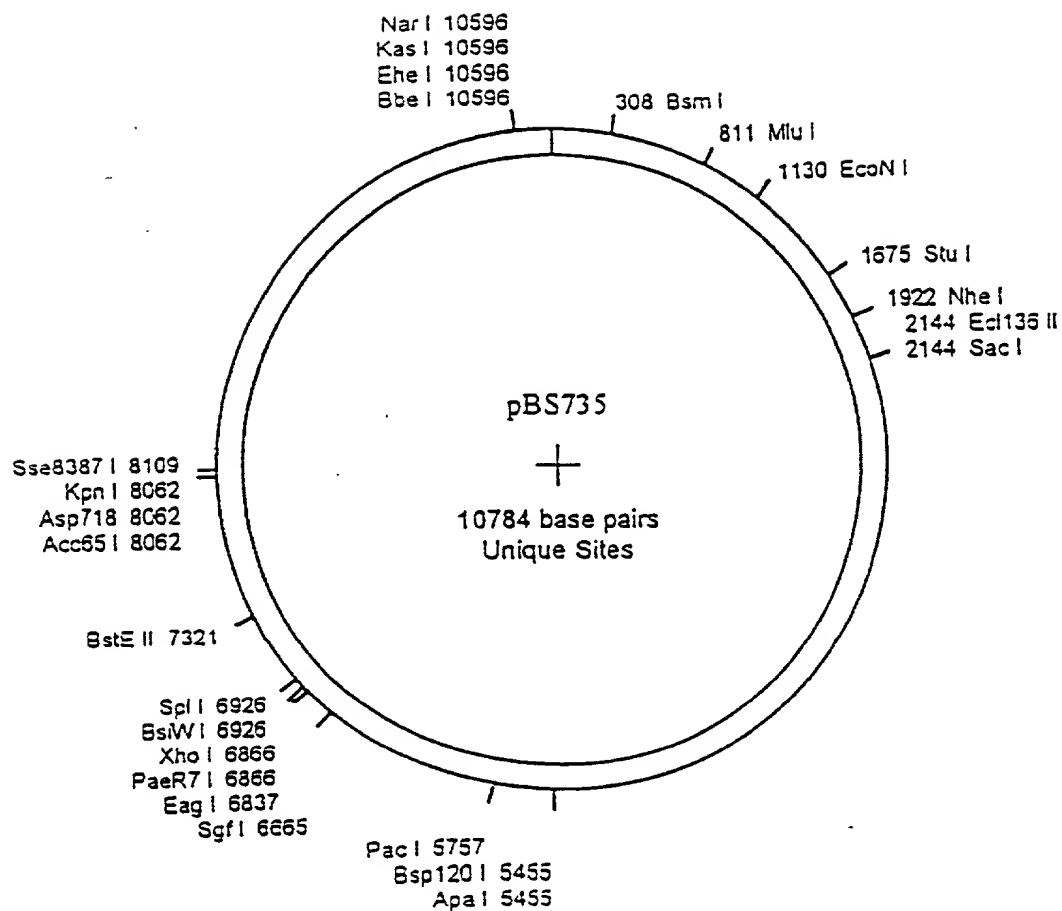


Figure 7

pBS740

9687 base pairs
Unique Sites

NarI 9499
KasI 9499
EheI 9499
BbeI 9499
256 SmaI
256 XmaI
308 BsmI
811 MluI
981 SexAI
1130 EcoNI
1675 StuI
1922 NheI
2144 Ecl136II
2144 SacI
3988 XcmI
NotI 5762
NcoI 5459
Bsp120I 5455
ApaI 5455
EagI 5763
PaeR7I 5769
XhoI 5769
PmlI 5820
BsiWI 5829
SplI 5829
BstEII 6224
Acc65I 6965
Asp718 6965
KpnI 6965
Sse8387I 7012
PstI 7013
AhdI 8272

Figure 8

[illegible]

The diagram illustrates the circular map of the **TTU51A QSEO #3** (11.5 kb) plasmid. The map includes the following features:

- Restriction Sites:** ClaI, XhoI, AvrII, KpnI, and BamHI.
- Gene Regions:** α -trichosanthin, Usp, and TMV RNA (+1).
- Gene Sizes:** 30K, 183/54K, and 126K.
- Plasmid Name:** TTU51A QSEO #3 (11.5 kb).
- Origin of Replication:** pBR322.
- Detailed View:** A 68 nt region is shown, containing the 126K gene and the SP6 promoter.

Figure 9

pBS723
3838 base pairs
Unique Sites

Enzyme	Position (bp)
Xmn I	3515
Aha II	3456
Sca I	3398
Fsp I	3140
Bsa I	2987
Ahd I	2915
AlwN I	2438
Dra III	220
BsaA I	223
Nae I	326
BstX I	653
Sac II	656
Not I	664
Eag I	665
Xba I	672
Spe I	678
Sma I	691
Xma I	691
BstS I	809
Hinc II	827
Sal I	827
Mun I	870
Bst1107 I	982
Sna I	982
Xca I	982
Mlu I	1108
BsrG I	1154
Nde I	1201
BspE I	1208
Msc I	1251
Hind III	1309
Sph I	1437
Nsi I	1439
Afl II	1522
Pst I	1584
Acc65 I	1629
Asp718	1629
Kpn I	1629

Figure 10

256 Sma I
256 Xma I
308 Bsm I

1675 Stu I

pBS731

Sse8387	1	7902
Kpn	1	7855
Asc713		7355
Acc65	1	7355

Spl I 6719
BsiWI 6719
Pml I 6710
Sal I 6544

3988 Xcm!

[illegible]

pBS740 AT #2441
(10.6 kb)

Restriction sites and positions (bp):

- BglII(3)
- NotI(53)
- NotI(909)
- EagI(910)
- XhoI(916)
- KpnI(2112)
- PstI(2160)
- SmaI(5090)
- SacI(6978)
- NcoI(10293)

Scale: 30K, 183/54K, 126K

Other labels: U5, pUC19

Figure 12

Nucleotide sequence of 740 AT #2441

ct tca ctt tcg ccg

ATG GCT CTA CCT AAC CAG CAA ACC GTG GAT TAC CCT AGC TTC AAG CTC GTT ATC GTT GGC
M A L P N Q Q T V D Y P S F K L V I V G

GAT GGA GGC ACA GGG AAG ACC ACA TTT GTA AAG AGA CAT CTT ACT GGA GAG TTT GAG AAG
D G G T G K T T F V K R H L T G E F E K

AAG TAT GAA CCC ACT ATT GGT GTT GAG GTT CAT CCT CTT GAT TTC TTC ACT AAC TGT GGC
K Y E P T I G V E V H P L D F F T N C G

AAG ATC CGT TTC TAC TGT TGG GAT ACT GCT GGC CAA GAG AAA TTT GGT GGT CTT AGG GAT
K I R F Y C W D T A G Q E K F G G L R D

GGT TAC TAC ATC CAT GGA CAA TGT GCT ATC ATC ATG TTT GAT GTC ACA GCA CGA CTG ACA
G Y Y I H G Q C A I I M F D V T A R L T

TAC AAG AAT GTT CCA ACA TGG CAC CGT GAT CTT TGC AGG GTT TGT GAA AAC ATC CCA ATT
Y K N V P T W H R D L C R V C E N I P I

GTT CTT TGT GGG AAT AAA GTT GAT GTG AAG AAC AGG CAA GTC AAG GCC AAG CAG GTA ACA
V L C G N K V D V K N R Q V K A K Q V T

TTC CAC AGG AAG AAG AAC CTC CAG TAT TAC GAG ATA TCT GCC AAG AGC AAC TAC AAC TTC
F H R K K N L Q Y Y E I S A K S N Y N F

GAG AAG CCA TTC TTG TAC CTT GCT AGA AAG CTC GCC GGG GAC GCT AAT CTT CAC TTT GTG
E K P F L Y L A R K L A G D A N L H F V

GAA TCA CCT GCC CTT GCT CCC CCG GAA GTT CAA ATC GAC TTG GCT GCT CAG CAG CAG CAT
E S P A L A P P E V Q I D L A A Q Q Q H

GAG GCG GAG CTT GCA GCA GCA GCA AGT CAG CCA CTT CCT GAT GAC GAT GAT GAC ACC TTC
E A E L A A A A S Q P L P D D D D D T F

GAG TAG AGA AAG AGA GAT GTG ATC TGT CAC TGA TTA CCC GTT AGG GCT TGT CTG AAC TTT
E

TTT TTG TTC ATG GTG CTA TTT TTA TGT GTC CGT ACT TTG AAA TGA ATC GAT GAC ATT AGT

AAT TTT CAT TTT TAA GTT TTT AAC TGT CGC TAT GAA AGT GAA AAC

Figure 13

Nucleotide sequence alignment of 740 AT #2441 to AF017991
A. thaliana salt stress inducible small GTP binding protein Ran1

740 AT #2441	1	CTTCAC TTTCGCCGATGGCTCTACCTAACCAGCAAACCGTGGATTACCCTAGCTTCAAGC	60
AF017991	67	CTTCAC TTTCGCCGATGGCTCTACCTAACCAGCAAACCGTGGATTACCCTAGCTTCAAGC	126
740 AT #2441	61	TCGTTATCGTTGGCGATGGAGGCACAGGGAAGACCACATTGTAAAGAGACATCTTACTG	120
AF017991	127	TCGTTATCGTTGGCGATGGAGGCACAGGGAAGACCACATTGTAAAGAGACATCTTACTG	186
740 AT #2441	121	GAGAGTTTGAGAAGAAGTATGAACCCACTATTGGTGTGAGGTTTCATCCTCTTGATTCT	180
AF017991	187	GAGAGTTTGAGAAGAAGTATGAACCCACTATTGGTGTGAGGTTTCATCCTCTTGATTCT	246
740 AT #2441	181	TCACTAAGTGTGGCAAGATCCGTTTCTACTGTTGGGATACTGCTGGCCAAGAGAAATTTG	240
AF017991	247	TCACTAAGTGTGGCAAGATCCGTTTCTACTGTTGGGATACTGCTGGCCAAGAGAAATTTG	306
740 AT #2441	241	GTGGTCTTAGGGATGGTTACTACATCCATGGACAATGTGCTATCATCATGTTTGATGTCA	300
AF017991	307	GTGGTCTTAGGGATGGTTACTACATCCATGGACAATGTGCTATCATCATGTTTGATGTCA	366
740 AT #2441	301	CAGCACGACTGACATACAAGAATGTTCCAACATGGCACCGTGATCTTTGCAGGGTTTGTG	360
AF017991	367	CAGCACGACTGACATACAAGAATGTTCCAACATGGCACCGTGATCTTTGCAGGGTTTGTG	426
740 AT #2441	361	AAAACATCCCAATTGTTCTTTGTGGGAATAAAGTTGATGTGAAGAACAGGCAAGTCAAGG	420
AF017991	427	AAAACATCCCAATTGTTCTTTGTGGGAATAAAGTTGATGTGAAGAACAGGCAAGTCAAGG	486
740 AT #2441	421	CCAAGCAGGTAACATTCACAGGAAGAAGAACTCCAGTATTACGAGATATCTGCCAAGA	480
AF017991	487	CCAAGCAGGTAACATTCACAGGAAGGAGGAAGTCCAGTATTACGAGATATCTGCCAAGA	546
740 AT #2441	481	GCAACTACAACCTTCGAGAAGCCATTCTTGTTACCTTGCTAGAAAGCTCGCCGGGGACGCTA	540
AF017991	547	GCAACTACAACCTTCGAGAAGCCATTCTTGTTACCTTGCTAGAAAGCTCGCCGGGGACGCTA	606
740 AT #2441	541	ATCTTCAC TTGTGGAATCACCTGCCCCTTGCTCCCCCGAAGTTCAAATCGACTTGGCTG	600
AF017991	607	ATCTTCAC TTGTGGAATCACCTGCCCCTTGCTCCCCCGAAGTTCAAATCGACTTGGCTG	666
740 AT #2441	601	CTCAGCAGCAGCATGAGGCGGAGCTTGACAGCAGCAGCAAGTCAGCCACTTCCTGATGACG	660
AF017991	667	CTCAGCAGCAGCATGAGGCGGAGCTTGACAGCAGCAGCAAGTCAGCCACTTCCTGATGACG	726
740 AT #2441	661	ATGATGACACCTTCGAGTAGAGAAAGAGAGATGTGATCTGTCACTGATTACCCGTTAGGG	720
AF017991	727	ATGATGACACCTTCGAGTAGAGAAAGAGAGATGTGATCTGTCACTGATTACCCGTTAGGG	786
740 AT #2441	721	CTTGTCTGAAC TTTTTT	738
AF017991	787	CTTGTCTGAAC TTTTTT	804

Figure 14

Nucleotide sequence alignment of 740 AT #2441 to L16787
N. tabacum small ras-like GTP-binding protein

740 AT #2441	15	ATGGCTCTACCTAACCAGCAAACCGTGGATTACCCTAGCTTCAAGCTCGTTATCGTTGGC	74
L16787	37	ATGGCTCTACCAAAACCAACAACTGTAGATTATCCAAGCTTCAAGCTTGAATCGTGGGC	96
740 AT #2441	75	GATGGAGGCACAGGAAGACCACATTTGTAAAGAGACATCTTACTGGAGAGTTTGAGAAG	134
L16787	97	GATGGAGGAAC TGGAAAACAAC TTTGTCAAGAGGCATCTTACTGGTGAATTTGAGAAG	156
740 AT #2441	135	AAGTATGAACCCACTATTGGTGTGGAGGTTTCATCCTCTTGATTCTTCACTAACTGTGGC	194
L16787	157	AAATATGAACCCACTATTGGTGTGGAGGTTTCATCCATTAGACTTCTTCACAAATTTGTGGG	216
740 AT #2441	195	AAGATCCGTTTCTACTGTTGGGATACTGCTGGCCAAGAGAAAATTTGGTGGTCTTAGGGAT	254
L16787	217	AAAATTCGCTTTTATTGCTGGGATACTGCTGGACAAGAGAAGTTTGGAGGTCTTCGGGAT	276
740 AT #2441	255	GGTTACTACATCCATGGACAATGTGCTATCATCATGTTTGATGTACAGCAGGACTGACA	314
L16787	277	GGTTACTACATTCATGGGCAATGCCAATTATCATGTTTGATGTTACAGCCCGTCTGACC	336
740 AT #2441	315	TACAAGAATGTTCCAACATGGCACCGTGATCTTTGCAGGGTTTGTGAAAACATCCCAATT	374
L16787	337	TACAAGAATGTTCTTACGTGGCATCGAGATCTCTGCAGGGTTTGTGAAAACATCCCAATT	396
740 AT #2441	375	GTTCTTTGTGGGAATAAAGTTGATGTGAAGAACAGGCAAGTCAAGGCCAAGCAGGTAACA	434
L16787	397	GTTCTTTGTGGAAACAAAGTTGATGTCAAGAACAGGCAGGTTAAGGCCAAGCAAGTTACC	456
740 AT #2441	435	TTCCACAGGAAGAAGAACCCTCCAGTATTACGAGATATCTGCCAAGAGCAACTACAAC TTC	494
L16787	457	TTCCACAGGAAGAAAAATTTGCAATAC TATGAGATCTCAGCAAAGAGTAACTACAAC TTT	516
740 AT #2441	495	GAGAAGCCATTCTTGTACCTTGCTAGAAAGCTCGCCGGGACGCTAATCTTCAC TTTGTG	554
L16787	517	GAGAAGCCTTTTCTGTACCTTGCCAGAAAGCTTGCTGGGGATGCTAATCTTCAC TTTGTG	576
740 AT #2441	555	GAATCACCTGCCCTTGCTCCCCCGGAAGTTCAAATCGACTTGGCTGCTCAGCAGCAGCAT	614
L16787	577	GAATCACCTGCACCTTGCTCCCCCTGAAGTACAAATTGATTTAGCTGCACAGCAACTGCAT	636
740 AT #2441	615	GAGGCGGAGCTTGCAGCAGCAGCAAGTCAGCCACTTCCTGATGACGATGATGACACCTTC	674
L16787	637	GAACAAGAGCTTTTGCAAGCCGCTGCGCACGCAC TTCCAGATGACGATGATGAAGCTTTT	696
740 AT #2441	675	GAGTAGA	681
L16787	697	GAATAGA	703

Figure 15

Amino acid sequence comparison of 740 AT #2441 to tobacco RAN-B1 GTP binding protein

Nt RAN-B1	MALPNQQTVDYPSFKLVIVGDGGTGKTTFVKRHLTGEFEKKYEPTIGVEVHPLDFFTNCG
740 AT #2441	MALPNQQTVDYPSFKLVIVGDGGTGKTTFVKRHLTGEFEKKYEPTIGVEVHPLDFFTNCG
Nt RAN-B1	KIRFYCWDTAGQEKFGGLRDGYIYHGQCAIMFDVTSTTDIQECSNMAP*SLQGL*KHSQ
	+ + + ++
740 AT #2441	KIRFYCWDTAGQEKFGGLRDGYIYHGQCAIMFDVTARLTYKNVPTWHR-DLCRVCENIP
Nt RAN-B1	LFFVGIKLM*KNRQVKAQ
	+ + +
740 AT #2441	IVLCGNKVDVKNRQVKAK

Figure 16

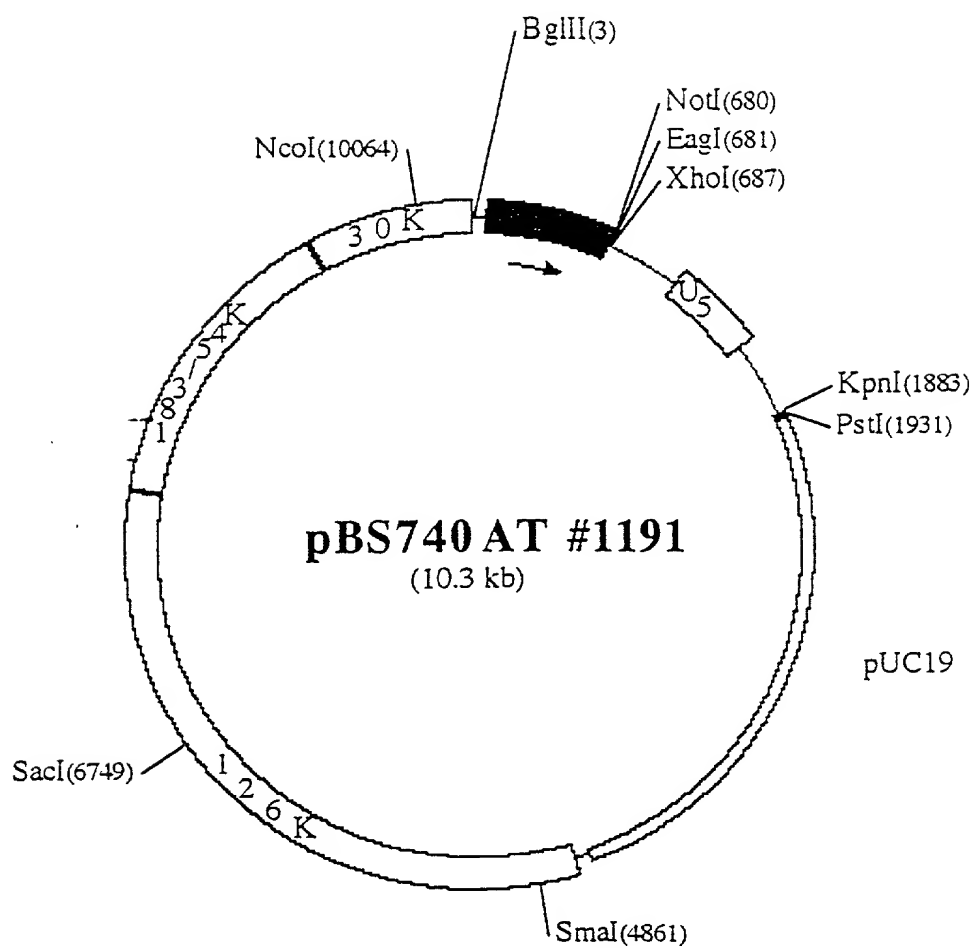


Figure 17

Nucleotide sequence of 740 AT #1191

GCT ACT ATG GTT GCC TCT CCG GCT CAG GCC ACT ATG GTC GCT CCT TTC AAC GGA CTT AAG
A T M V A S P A Q A T M V A P F N G L K

TCC TCC GCT GCC TTC CCA GCC ACC CGC AAG GCT AAC AAC GAC ATT ACT TCC ATC ACA AGC
S S A A F P A T R K A N N D I T S I T S

AAC GGC GGA AGA GTT AAC TGC | ATG CAG GTG TGG CCT CCG ATT GGA AAG AAG AAG TTT GAG
N G G R V N C | M Q V W P P I G K K K F E

ACT CTC TCT TAC CTT CCT GAC CTT ACC GAT TCC GAA TTG GCT AAG GAA GTT GAC TAC CTT
T L S Y L P D L T D S E L A K E V D Y L

ATC CGC AAC AAG TGG ATT CCT TGT GTT GAA TTC GAA GT
I R N K W I P C V E F E V

Figure 18

Figure 19

Nucleotide sequence alignment of 740 AT #855 to *Arabidopsis thaliana*
HAT7 homeobox protein ORF (U09340)

HAT7	GAA ACG ACG TCG GCT AGT TAT TGG GCA TGG CCT GAC CAG CAG CAA
	E T T S A S Y W A W P D Q Q Q
HAT7	CAA CAT CAC AAT CAT CAT CAG TTC AAT TGA tcatattgtctaagaaca
	Q H H N H H Q F N *
HAT7	acatcatactcatcttgatatcattattatcatcaaaagaaaattccgtagattttttta
HAT7	ataagtattttcaaattatttggcacggtttaaaattaattaattgggttattatgttt
740 AT #855	acttgatctgtttcataactaaaaccaaaactcatgtttgttccactccaaacacaaacaca
HAT7	- acttgatctgtttcataactaaaaccaaaactcatgtttgttccactccaaacacaaacaca
740 AT #855	gcagtaatcaaaaatcgtctttataacaaaaaggaaatgcaacaaaacagaagaacaact
HAT7	gcagtaatcaaaaatcgtctttataacaaaaaggaaatgcaacaaaacagaagaacaact
740 AT #855	aagtagtaggcaagattcttcttcactcgtcttcttggctacggagcc
HAT7	aagtagtaggcaagattcttcttcactcgtcttcttggctacggagcc

Figure 20

Nucleotide sequence alignment of 740 AT #909 to *H. sapiens* S56985 ribosomal protein L19
[human, breast cancer cell line, MCF-7]

740 AT #909	1	GAAGCGGCTCGCCGCATCAGTGATGAAGTGCGGGAAGGGCAAAGTTTGGCTCGATCCCAA	60
S56985	32	GAAGAGGCTCGCCTCTAGTGTCTCCGCTGTGGCAAGAAGAAGGTCTGGTTAGACCCCAA	91
740 AT #909	61	CGAAAGCTCCGACATCTCCATGGCCAATTCCCGCCAAAACATCAGGAAGCTTGTGAAGGA	120
S56985	92	TGAGACCAATGAAATCGCCAATGCCAACTCCCGTCAGCAGATCCGGAAGCTCATCAAAGA	151
740 AT #909	121	TGGTTTTCATCATCAGGAAGCCAACCAAGATTCACTCTCGTTCCAGAGCTCGCAAAATGAA	180
S56985	152	TGGGCTGATCATCCGCAAGCCTGTGACGGTCCATTCCCGGGCTCGATGCCGGAACAAACAC	211
740 AT #909	181	GATTGCCAAGATGAAGGGTCGTCACTCTGGATACGGTAAGAGGAAGGGTACCCGTGAAGC	240
S56985	212	CTTGGCCCCGCCGAAGGGCAGGCACATGGGCATAGGTAAGCGGAAGGGTACAGCCAATGC	271
740 AT #909	241	TAGGTTGCCAACAAGGTACTGTGGATGCGTAGGATGCGTGTTCTTAGGCGTCTGTTGAA	300
S56985	272	CCGAATGCCAGAGAAGGTCACATGGATGAGGAGAATGAGGATTTTGCGCCGGCTGCTCAG	331
740 AT #909	301	GAAATACAGAGAGACGAAGAAGATTGACAAGCACATGTACCATGACATGTACATGCGTGT	360
S56985	332	AAGATACCGTGAATCTAAGAAGATCGATCGCCACATGTATCACAGCCTGTACCTGAAGGT	391
740 AT #909	361	TAAGGGTAATGTGTTCAAGAACAAGCGTGTCTTGATGGAGAGTATCCACAAGTCAAAGGC	420
S56985	392	GAAGGGGAATGTGTTCAAAAACAAGCGGATTCTCATGGAACACATCCACAAGCTGAAGGC	451
740 AT #909	421	TTAGAAGCTAGGGGAGAA	438
S56985	452	AGACAAGGCCCGCAAGAA	469

Figure 22

Amino acid sequence alignment of 740 AT #909 to human P14118 60S ribosomal protein L19

740 AT #909	1	KRLAASVMKCGKGVWLDPNESDISMANSRQNIRKLVDGFIIRKPTKIHSR SRARKMK	60
		KRLA+SV++CGK KVLDPNE+++I+ ANSRQ IRKL+KDG IIRKP +HSR+R RK	
Human P14118	8	KRLASSVLRCGKKKVWLDPNETNEIANANSRQQIRKLIKDGLIIRKPVTVHSRARC RKNT	67
740 AT #909	61	IAKMKGRHSGYGKRKG TREARLPTKVLWMRRMRVLRLLKKYRETKKIDKHMYHDMYMRV	120
		+A+ KGRH G GKRKGT AR+P KV WMRRMR+LRLL++YRE+KKID+HMYH +Y++V	
Human P14118	68	LARRKGRHMGIGKRKGTANARMPEKVTWMRRMRILRLLRRYRESKKIDRHMYHSLYLKV	127
740 AT #909	121	KGNVFKNKRVLME SIHKS KA*KLGEK	146
		KGNVFKNKR+LME IHK KA K +K	
Human P14118	128	KGNVFKNKRILMEHIHKLKADKARKK	153

Figure 23